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(54) **Title:** HIGH EFFICIENCY GENE TRANSFER AND EXPRESSION IN MAMMALIAN CELLS BY A MULTIPLE TRANSFECTION PROCEDURE OF MAR SEQUENCES

(57) **Abstract:** The present invention relates to purified and isolated DNA sequences having protein production increasing activity and more specifically to the use of matrix attachment regions (MARs) for increasing protein production activity in a eukaryotic cell. Also disclosed is a method for the identification of said active regions, in particular MAR nucleotide sequences, and the use of these characterized active MAR sequences in a new multiple transfection method.

HIGH EFFICIENCY GENE TRANSFER AND EXPRESSION IN MAMMALIAN CELLS BY A MULTIPLE TRANSFECTION PROCEDURE OF MAR SEQUENCES

FIELD OF THE INVENTION

The present invention relates to purified and isolated DNA sequences having protein production increasing activity and more specifically to the use of matrix attachment regions (MARs) for increasing protein production activity in a eukaryotic cell. Also disclosed is a method for the identification of said active regions, in particular MAR nucleotide sequences, and the use of these characterized active MAR sequences in a new multiple transfection method.

BACKGROUND OF THE INVENTION

Nowadays, the model of loop domain organization of eukaryotic chromosomes is well accepted (Boulikas T, "Nature of DNA sequences at the attachment regions of genes to the nuclear matrix", *J. Cell Biochem.*, 52:14-22, 1993). According to this model chromatin is organized in loops that span 50-100 kb attached to the nuclear matrix, a proteinaceous network made up of RNPs and other nonhistone proteins (Bode J, Stengert-Iber M, Kay V, Schalke T and Dietz-Pfeilstetter A, *Crit. Rev. Euk. Gene Exp.*, 6:115-138, 1996).

The DNA regions attached to the nuclear matrix are termed SAR or MAR for respectively scaffold (during metaphase) or matrix (interphase) attachment regions (Hart C and Laemmli U (1998), "Facilitation of chromatin dynamics by SARs" *Curr Opin Genet Dev* 8, 519-525.)

As such, these regions may define boundaries of independent chromatin domains, such that only the encompassing cis-regulatory elements control the expression of the genes within the domain.

However, their ability to fully shield a chromosomal locus from nearby chromatin elements, and thus confer position-independent gene expression, has not been seen in stably transfected cells (Poljak L, Seum C, Mattioni T and Laemmli U. (1994) "SARs stimulate but do not confer position independent gene expression", *Nucleic Acids Res* 22, 4386-4394). On the other hand, MAR (or S/MAR) sequences have been shown to interact with enhancers to increase local chromatin accessibility (Jenuwein T, Forrester W, Fernandez-Herrero L, Laible G, Dull M, and Grosschedl R. (1997) "Extension of chromatin accessibility by nuclear matrix attachment regions" *Nature* 385, 269-272). Specifically, MAR elements can enhance expression of heterologous genes in cell culture lines (Kalos M and Fournier R (1995) "Position-independent transgene expression mediated by boundary elements from the apolipoprotein B chromatin domain" *Mol Cell Biol* 15,198-207), transgenic mice (Castilla J, Pintado B, Sola, I, Sanchez-Morgado J, and Enjuanes L (1998) "Engineering passive immunity in transgenic mice secreting virus-neutralizing antibodies in milk" *Nat Biotechnol* 16, 349-354) and plants (Allen G, Hall GJ, Michalowski S, Newman W, Spiker S, Weissinger A, and Thompson W (1996), "High-level transgene expression in plant cells: effects of a strong scaffold attachment region from tobacco" *Plant Cell* 8, 899-913). The utility of MAR sequences for developing improved vectors for gene therapy is also recognized (Agarwal M, Austin T, Morel F, Chen J, Bohnlein E, and Plavec I (1998), "Scaffold attachment region-mediated enhancement of retroviral vector expression in primary T

cells" *J Virol* 72, 3720-3728).

Recently, it has been shown thatchromatin-structure modifying sequences including MARs, as exemplified by the chicken lysozyme 5' MAR is able to significantly enhance reporter expression in pools of stable Chinese Hamster Ovary (CHO) cells (Zahn-Zabal M, et al., "Development of stable cell lines for production or regulated expression using matrix attachment regions" *J Biotechnol*, 2001, 87(1): p. 29-42). This property was used to increase the proportion of high-producing clones, thus reducing the number of clones that need to be screened. These benefits have been observed both for constructs with MARs flanking the transgene expression cassette, as well as when constructs are co-transfected with the MAR on a separate plasmid. However, expression levels upon co-transfection with MARs were not as high as those observed for a construct in which two MARs delimit the transgene expression unit. A third and preferable process was shown to be the transfection of transgenes with MARs both linked to the transgene and on a separate plasmid (Girod et al., submitted for publication). However, one persisting limitation of this technique is the quantity of DNA that can be transfected per cell. Many multiples transfection protocols have been developed in order to achieve a high transfection efficiency to characterize the function of genes of interest. The protocol applied by Yamamoto et al, 1999 ("High efficiency gene transfer by multiple transfection protocol", *Histochem. J.* 31(4), 241-243) leads to a transfection efficiency of about 80 % after 5 transfections events, whereas the conventional transfection protocol only achieved a rate of <40%. While this technique may be useful when one wishes to increase the proportion of expressing cells, it does not lead to cells with a higher intrinsic productivity. Therefore, it cannot be used to generate high producer monoclonal cell lines. Hence, the previously described technique has two major drawbacks:

i) this technique does not generate a homogenous population of transfected cells, since it cannot favour the integration of further gene copy, nor does it direct the transgenes to favorable chromosomal loci,

ii) the use of the same selectable marker in multiple transfection events does not permit the selection of doubly or triply transfected cells.

In patent application WO02/074969, the utility of MARs for the development of stable eukaryotic cell lines has also been demonstrated. However, this application does not disclose neither any conserved homology for MAR DNA element nor any technique for predicting the ability for a DNA sequence to be a MAR sequence.

In fact no clear-cut MAR consensus sequence has been found (Boulikas T, "Nature of DNA sequences at the attachment regions of genes to the nuclear matrix", *J. Cell Biochem.*, 52:14-22, 1993) but evolutionarily, the structure of these sequences seem to be functionally conserved in eukaryotic genomes, since animal MARs can bind to plant nuclear scaffolds and vice versa (Mielke C, Kohwi Y, Kohwi-Shigematsu T and Bode J, "Hierarchical binding of DNA fragments derived from scaffold-attached regions: correlation of properties in vitro and function in vivo", *Biochemistry*, 29:7475-7485, 1990) .

The identification of MARs by biochemical studies is a long and unpredictable process; various results can be obtained depending on the assay (Razin SV, "Functional architecture of chromosomal DNA domains", *Crit Rev Eukaryot Gene Expr.*, 6:247-269, 1996). Considering the huge number of expected MARs in a eukaryotic genome and the amount of sequences issued from genome projects, a tool able to filter potential MARS in order to perform targeted experiments would be greatly useful.

Currently two different predictive tools for MARs are available via the Internet. The fist one, MAR-Finder (http://futuresoft.org/MarFinder; Singh GB, Kramer JA and Krawetz SA, "Mathematical model to predict regions of chromatin attachment to the nuclear matrix", *Nucleic Acid Research*, 25:1419-1425, 1997) is based on set of patterns identified within several MARs and a statistical analysis of the co-occurrence of these patterns. MAR-Finder predictions are dependent of the sequence context, meaning that predicted MARs depend on the context of the submitted sequence. The other predictive software, SMARTest (http://www. genomatix.de; Frisch M, Frech K, Klingenhoff A, Cartharius K, Liebich I and Werner T, "In silico prediction of scaffold/matrix attachment regions in large genomic sequences", *Genome Research*, 12:349-354, 2001), use weight-matrices derived from experimentally identified MARs. SMARTest is said to be suitable to perform large-scale analyses. But actually aside its relative poor specificity, the amount of hypothetical MARs rapidly gets huge when doing large scale analyses with it, and in having no way to increase its specificity to restrain the number of hypothetical MARs, SMARTest becomes almost useless to screen for potent MARs form large DNA sequences.
Some other softwares, not available via the Internet, also exists; they are based as well on the frequency of MAR motifs (MRS criterion;Van Drunen CM et al., "A bipartite sequence element associated with matrix/scaffold attachment regions", *Nucleic Acids Res*, 27:2924-2930, 1999), (ChrClass; Glazko GV et al., "Comparative study and prediction of DNA fragments associated with various elements of the nuclear matrix", *Biochim. Biophys. Acta*, 1517:351-356, 2001) or based on the identification of sites of stress-induced DNA duplex (SIDD; Benham C and al., "Stress-induced duplex DNA destabilization in scaffold/matrix attachment regions", *J. Mol. Biol.*, 274:181-196, 1997). However, their suitability to analyze complete genome sequences remains unknown, and whether these tools may allow the identification of protein production-increasing sequences has not been reported.

Furthermore, due to the relatively poor specificity of these softwares (Frisch M, Frech K, Klingenhoff A, Cartharius K, Liebich I and Werner T, "In silico prediction of scaffold/matrix attachment regions in large genomic sequences", *Genome Research*, 12:349-354, 2001), the amount of hypothetical MARs identified in genomes rapidly gets unmanageable when doing large scale analyses, especially if most of these have no or poor activity in practice. Thus, having no way to increase prediction specificity to restrain the number of hypothetical MARs, many of the available programs become almost useless to identify potent genetic elements in view of efficiently increasing recombinant protein production.

Since all the above available predictive methods have some drawbacks that prevent large-scale analyses of genomes to identify reliably novel and potent MARs, the object of this invention is to 1) understand the functional features of MARs that allow improved recombinant protein expression; 2) get a new Bioinformatic tool compiling MAR structural features as a prediction of function, in order to 3) perform large scale analyses of genomes to identify novel and more potent MARs, and, finally 4) to demonstrate improved efficiency to increase the production of recombinant proteins from eukaryotic cells or organisms when using the newly identified MAR sequences.

SUMMARY OF THE INVENTION

This object has been achieved by providing an improved and reliable method for the identification of DNA sequences having protein production increasing activity, in

particular MAR nucleotide sequences, and the use of these characterized active MAR sequences in a new multiple transfection method to increase the production of recombinant proteins in eukaryotic cells.

BRIEF DESCRIPTION OF THE FIGURES

Fig. 1 shows the distribution plots of MARs and non-MARs sequences. Histograms are density plots (relative frequency divided by the bin width) relative to the score of the observed parameter. The density histogram for human MARs in the SMARt DB database is shown in black, while the density histogram for the human chromosome 22 are in grey.

Fig. 2 shows Scatterplots of the four different criteria used by SMAR Scan® and the AT-content with human MARs from SMARt DB.

Fig. 3 shows the distribution plots of MAR sequences by organism. MAR sequences from SMARt DB of other organisms were retrieved and analyzed. The MAR sequences density distributions for the mouse, the chicken, the sorghum bicolor and the human are plotted jointly.

Fig. 4 shows SMAR Scan® predictions on human chromosome 22 and on shuffled chromosome 22. Top plot : Average number of hits obtained by SMAR Scan® with five: rubbled, scrambled, shuffled within nonoverlapping windows of 10 bp, order 1 Markov chains model and with the native chromosome 22. Bottom plot: Average number of MARs predicted by SMAR Scan® in five: rubbled, scrambled, shuffled within non-overlapping windows of 10 bp, order 1 Markov chains model and with the native chromosome 22.

Fig. 5 shows the dissection of the ability of the chicken lysozyme gene 5'-MAR to stimulate transgene expression in CHO-DG44 cells. Fragments B, K and F show the highest ability to stimulate transgene expression. The indicated relative strength of the elements was based on the number of high-expressor cells.

Fig. 6 shows the effect of serial-deletions of the 5'-end (upper part) and the 3'-end (lower part) of the 5'-MAR on the loss of ability to stimulate transgene expression. The transition from increased to decreased activity coincide with B-, K- and F-fragments.

Fig. 7 shows that portions of the F fragment significantly stimulate transgene expression. The F fragment regions indicated by the light grey arrow were multimerized, inserted in pGEGFP Control and transfected in CHO cells. The element that displays the highest activity is located in the central part of the element and corresponds to fragment FIII (black bar labelled minimal MAR). In addition, an enhancer activity is located in the 3'-flanking part of the FIII fragment (dark grey bar labelled MAR enhancer).

Fig. 8 shows a map of locations for various DNA sequence motifs within the *cLysMAR*. Fig. 8 (B) represents a Map of locations for various DNA sequence motifs within the cLysMAR. Vertical lines represent the position of the computer-predicted sites or sequence motifs along the 3034 base pairs of the cLysMAR and its active regions, as presented in Fig. 5. The putative transcription factor sites, (MEF2 05, Oct-1, USF-02, GATA, NFAT) for activators and (CDP, SATB1, CTCF, ARBP/MeCP2) for repressors of transcription, were identified using MatInspector (Genomatix), and CpG islands were identifed with CPGPLOT. Motifs previously associated with MAR elements are labelled

in black and include CpG dinucleotides and CpG islands, unwinding motifs (AATATATT and AATATT), poly As and Ts, poly Gs and Cs, Drosophila topoisomerase II binding sites (GTNWAYATTNATTNATNNR) which had identity to the 6 bp core and High mobility group I (HMG-I/Y) protein binding sites. Other structural motifs include nucleosome-binding and nucleosome disfavouring sites and a motif thought to relieve the superhelical strand of DNA. Fig. 8(A) represents the comparison of the ability of portions of the cLysMAR to activate transcription with MAR prediction score profiles with MarFinder. The top diagram shows the MAR fragment activity as in Fig. 5, while the middle and bottom curves show MARFinder-predicted potential for MAR activity and for bent DNA structures respectively.

Fig. 9 shows the correlation of DNA physico-chemical properties with MAR activity. Fig. 9(A), represents the DNA melting temperature, double helix bending, major groove depth and minor groove width profiles of the 5'-MAR and were determined using the algorithms of Levitsky et al (Levitsky VG, Ponomarenko MP, Ponomarenko JV, Frolov AS, Kolchanov NA "Nucleosomal DNA property database", *Bioinformatics*, 15; 582592, 1999). The most active B, K and F fragments depicted at the top are as shown as in Figure 1. Fig. 9(B), represents the enlargement of the data presented in panel A to display the F fragment map aligned with the tracings corresponding to the melting temperature (top curve) and DNA bending (bottom curve). The position of the most active FIB fragment and protein binding site for specific transcription factors are as indicated.

Fig. 10 shows the distribution of putative transcription factor binding sites within the 5'-cLysMAR. Large arrows indicate the position of the CUE elements as identified with SMAR Scan®.

Fig. 11 shows the scheme of assembly of various portions of the MAR. The indicated portions of the cLysMAR were amplified by PCR, introducing BglII-BamHI linker elements at each extremity, and assembled to generate the depicted composite elements. For instance, the top construct consists of the assembly of all CUE and flanking sequences at their original location except that BglI-BamHII linker sequences separate each element.

Fig. 12 represents the plasmid maps.

Fig. 13 shows the effect of re-transfecting primary transfectants on GFP expression. Cells (CHO-DG44) were co-transfected with pSV40EGFP (left tube) or pMAR-SV40EGFP (central tube) and pSVneo as resistance plasmid. Cells transfected with pMAR-SV40EGFP were re-transfected 24 hours later with the same plasmid and a different selection plasmid, pSVpuro (right tube). After two weeks selection, the phenotype of the stably transfected cell population was analysed by FACS.

Fig. 14 shows the effect of multiple load of MAR-containing plasmid. The pMAR-SV40EGFP/ pMAR-SV40EGFP secondary transfectants were used in a third cycle of transfection at the end of the selection process. The tertiary transfection was accomplished with pMAR or pMAR-SV40EGFP to give tertiary transfectants. After 24 hours, cells were transfected again with either plasmid, resulting in the quaternary transfectants (see Table 4).

Fig. 15 shows comparative performance of SMAR prediction algorithms exemplified by region WP18A10A7. (A) SMAR Scan® analysis was performed with default settings. (B) SIDD analysis (top curve and left-hand side scale), and the attachment of several

DNA fragments to the nuclear matrix in vitro (bar-graph, right-hand side scale) was taken from Goetze et al (Goetze S, Gluch A, Benham C, Bode J, "Computational and in vitro analysis of destabilized DNA regions in the interferon gene cluster: potential of predicting functional gene domains." *Biochemistry*, 42:154-166, 2003).

Fig. 16 represents the results of a a gene therapy-like protocol using MARs. The group of mice injected by MAR-network, induced from the beginning of the experiment, display a better induction of the hematocrit in comparison of mice injected by original network without MAR. After 2 months, hematocrits in "MAR-containing group" is still at values higher (65%) than normal hematocrit levels (45-55%).

Fig. 17 represents the scatterplot for the 1757 S/MAR sequences of the AT (top) and TA (bottom) dinucleotide percentages versus the predicted DNA bending as computed by SMAR Scan®.

Fig. 18 represents the dinucleotide percentage distribution plots over the 1757 non-S/MARs sequences.

Fig.19 shows the effect of various S/MAR elements on the production of recombinant green fluorescent protein (GFP). Populations of CHO cells transfected with a GFP expression vector containing or a MAR element, as indicated, were analyzed by a fluorescence-activated cell sorter (FACS®), and typical profiles are shown. The profiles display the cell number counts as a function of the GFP fluorescence levels.

Fig. 20 depicts the effect of the induction of hematocrit in mice injected by MAR-network.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to a purified and isolated DNA sequence having protein production increasing activity characterized in that said DNA sequence comprises at least one bent DNA element, and at least one binding site for a DNA binding protein.

Certain sequences of DNA are known to form a relatively "static curve", where the DNA follows a particular 3-dimensional path. Thus, instead of just being in the normal B-DNA conformation ("straight"), the piece of DNA can form a flat, planar curve also defined as bent DNA (Marini, *et al.*, 1982 "Bent helical structure in kinetoplast DNA", *Proc. Natl. Acad. Sci. USA*, 79: 7664-7664).

Surprisingly, Applicants have shown that the bent DNA element of a purified and isolated DNA sequence having protein production increasing activity of the present invention usually contains at least 10% of dinucleotide TA, and/or at least 12% of dinucleotide AT on a stretch of 100 contiguous base pairs. Preferably, the bent DNA element contains at least 33% of dinucleotide TA, and/or at least 33% of dinucleotide AT on a stretch of 100 contiguous base pairs. These data have been obtained by the method described further.

According to the present invention, the purified and isolated DNA sequence usually comprises a MAR nucleotide sequence selected from the group comprising the sequences SEQ ID Nos 1 to 27 or a cLysMAR element or a fragment thereof. Preferably, the purified and isolated DNA sequence is a MAR nucleotide sequence

selected from the group comprising the sequences SEQ ID Nos 1 to 27, more preferably the sequences SEQ ID Nos 24 to 27.

Encompassed by the present invention are as well complementary sequences of the above-mentioned sequences SEQ ID Nos 1 to 27 and the cLysMAR element or fragment, which can be produced by using PCR or other means.

An "element" is a conserved nucleotide sequences that bears common functional properties (i.e. binding sites for transcription factors) or structural (i.e. bent DNA sequence) features.

A part of sequences SEQ ID Nos 1 to 27 and the cLysMAR element or fragment refers to sequences sharing at least 70% nucleotides in length with the respective sequence of the SEQ ID Nos 1 to 27. These sequences can be used as long as they exhibit the same properties as the native sequence from which they derive. Preferably these sequences share more than 80%, in particular more than 90% nucleotides in length with the respective sequence of the SEQ ID Nos 1 to 27.

The present invention also includes variants of the aforementioned sequences SEQ ID Nos 1 to 27 and the cLysMAR element or fragment, that is nucleotide sequences that vary from the reference sequence by conservative nucleotide substitutions, whereby one or more nucleotides are substituted by another with same characteristics.

The sequences SEQ ID Nos 1 to 23 have been identified by scanning human chromosome 1 and 2 using SMAR Scan®, showing that the identification of novel MAR sequences is feasible using the tools reported thereafter whereas SEQ ID No 24 to 27 have been identified by scanning the complete human genome using the combined SMAR Scan® method.

In a first step, the complete chromosome 1 and 2 were screened to identify bent DNA element as region corresponding to the highest bent, major groove depth, minor groove width and lowest melting temperature as shown in figure 3. In a second step, this collection of sequence was scanned for binding sites of regulatory proteins such as SATB1, GATA, etc. as shown in the figure 8B) yielding sequences SEQ ID 1-23. Furthermore, sequences 21-23 were further shown to be located next to known gene from the Human Genome Data Base.

With regard to SEQ ID No 24 to 27 these sequences have been yielded by scanning the human genome according to the combined method and were selected as examples among 1757 MAR elements so detected.

Molecular chimera of MAR sequences are also considered in the present invention. By molecular chimera is intended a nucleotide sequence that may include a functional portion of a MAR element and that will be obtained by molecular biology methods known by those skilled in the art.

Particular combinations of MAR elements or fragments or sub-portions thereof are also considered in the present invention. These fragments can be prepared by a variety of methods known in the art. These methods include, but are not limited to, digestion with restriction enzymes and recovery of the fragments, chemical synthesis or polymerase chain reactions (PCR).
Therefore, particular combinations of elements or fragments of the sequences SEQ ID

Nos 1 to 27 and cLysMAR elements or fragments are also envisioned in the present invention, depending on the functional results to be obtained. Elements of the cLysMAR are e.g. the B, K and F regions as described in WO 02/074969, the disclosure of which is hereby incorporated herein by reference, in its entirety. The preferred elements of the cLysMAR used in the present invention are the B, K and F regions. Only one element might be used or multiple copies of the same or distinct elements (multimerized elements) might be used (see Fig. 8 A)).

By fragment is intended a portion of the respective nucleotide sequence. Fragments of a MAR nucleotide sequence may retain biological activity and hence bind to purified nuclear matrices and/or alter the expression patterns of coding sequences operably linked to a promoter. Fragments of a MAR nucleotide sequence may range from at least about 100 to 1000 bp, preferably from about 200 to 700 bp, more preferably from about 300 to 500 bp nucleotides. Also envisioned are any combinations of fragments, which have the same number of nucleotides present in a synthetic MAR sequence consisting of natural MAR element and/or fragments. The fragments are preferably assembled by linker sequences. Preferred linkers are BglII-BamHI linker.

"Protein production increasing activity" refers to an activity of the purified and isolated DNA sequence defined as follows: after having been introduced under suitable conditions into a eukaryotic host cell, the sequence is capable of increasing protein production levels in cell culture as compared to a culture of cell transfected without said DNA sequence. Usually the increase is 1.5 to 10 fold, preferably 4 to 10 fold. This corresponds to a production rate or a specific cellular productivity of at least 10 pg per cell per day (see Example 11 and Fig.13).

As used herein, the following definitions are supplied in order to facilitate the understanding of this invention.

"Chromatin" is the protein and nucleic acid material constituting the chromosomes of a eukaryotic cell, and refers to DNA, RNA and associated proteins.

A "chromatin element" means a nucleic acid sequence on a chromosome having the property to modify the chromatine structure when integrated into that chromosome.

"Cis" refers to the placement of two or more elements (such as chromatin elements) on the same nucleic acid molecule (such as the same vector, plasmid or chromosome).

"Trans" refers to the placement of two or more elements (such as chromatin elements) on two or more different nucleic acid molecules (such as on two vectors or two chromosomes).

Chromatin modifying elements that are potentially capable of overcoming position effects, and hence are of interest for the development of stable cell lines, include boundary elements (BEs), matrix attachment regions (MARs), locus control regions (LCRs), and universal chromatin opening elements (UCOEs).

Boundary elements ("BEs"), or insulator elements, define boundaries in chromatin in many cases (Bell A and Felsenfeld G. 1999; "Stopped at the border: boundaries and insulators, *Curr Opin Genet Dev* 9, 191-198) and may play a role in defining a transcriptional domain in vivo. BEs lack intrinsic promoter/enhancer activity, but rather are thought to protect genes from the transcriptional influence of regulatory elements in the surrounding chromatin. The enhancer-block assay is commonly used to identify

insulator elements. In this assay, the chromatin element is placed between an enhancer and a promoter, and enhancer-activated transcription is measured. Boundary elements have been shown to be able to protect stably transfected reporter genes against position effects in Drosophila, yeast and in mammalian cells. They have also been shown to increase the proportion of transgenic mice with inducible transgene expression.

Locus control regions ("LCRs") are cis-regulatory elements required for the initial chromatin activation of a locus and subsequent gene transcription in their native locations (Grosveld, F. 1999, "Activation by locus control regions?" *Curr Opin Genet Dev* 9, 152-157). The activating function of LCRs also allows the expression of a coupled transgene in the appropriate tissue in transgenic mice, irrespective of the site of integration in the host genome. While LCRs generally confer tissue-specific levels of expression on linked genes, efficient expression in nearly all tissues in transgenic mice has been reported for a truncated human T-cell receptor LCR and a rat LAP LCR. The most extensively characterized LCR is that of the globin locus. Its use in vectors for the gene therapy of sickle cell disease and (3-thalassemias is currently being evaluated.

"MARs", according to a well-accepted model, may mediate the anchorage of specific DNA sequence to the nuclear matrix, generating chromatin loop domains that extend outwards from the heterochromatin cores. While MARs do not contain any obvious consensus or recognizable sequence, their most consistent feature appears to be an overall high A/T content, and C bases predominating on one strand (Bode J, Schlake T, RiosRamirez M, Mielke C, Stengart M, Kay V and KlehrWirth D, "Scaffold/matrix-attached regions: structural propreties creating transcriptionally active loci",*Structural and Functional Organization of the Nuclear Matrix: International Review of Citology*, 162A:389453, 1995). These regions have a propensity to form bent secondary structures that may be prone to strand separation. They are often referred to as base-unpairing regions (BURs), and they contain a core-unwinding element (CUE) that might represent the nucleation point of strand separation (Benham C and al., Stress induced duplex DNA destabilization in scaffold/matrix attachment regions, *J. Mol. Biol.*, 274:181-196, 1997). Several simple AT-rich sequence motifs have often been found within MAR sequences, but for the most part, their functional importance and potential mode of action remain unclear. These include the A-box (AATAAAYAAA), the T-box (TTWTWTTWTT), DNA unwinding motifs (AATATATT, AATATT), SATB1 binding sites (H-box, A/T/C25) and consensus Topoisomerase II sites for vertebrates (RNYNNCNNGYNGKTNYNY) or Drosophila (GTNWAYATTNATNNR).

Ubiquitous chromatin opening elements ("UCOEs", also known as "ubiquitously-acting chromatin opening elements") have been reported in WO 00/05393.

An "enhancer" is a nucleotide sequence that acts to potentiate the transcription of genes independent of the identity of the gene, the position of the sequence in relation to the gene, or the orientation of the sequence. The vectors of the present invention optionally include enhancers.

A "gene" is a deoxyribonucleotide (DNA) sequence coding for a given mature protein. As used herein, the term "gene" shall not include untranslated flanking regions such as RNA transcription initiation signals, polyadenylation addition sites, promoters or enhancers.

A "product gene" is a gene that encodes a protein product having desirable characteristics such as diagnostic or therapeutic utility. A product gene includes, e. g.,

structural genes and regulatory genes.

A "structural gene" refers to a gene that encodes a structural protein. Examples of structural genes include but are not limited to, cytoskeletal proteins, extracellular matrix proteins, enzymes, nuclear pore proteins and nuclear scaffold proteins, ion channels and transporters, contractile proteins, and chaperones. Preferred structural genes encode for antibodies or antibody fragments.

A "regulatory gene" refers to a gene that encodes a regulatory protein. Examples of regulatory proteins include, but are not limited to, transcription factors, hormones, growth factors, cytokines, signal transduction molecules, oncogenes, proto-oncogenes, transmembrane receptors, and protein kinases.

"Orientation" refers to the order of nucleotides in a given DNA sequence. For example, an inverted orientation of a DNA sequence is one in which the 5' to 3' order of the sequence in relation to another sequence is reversed when compared to a point of reference in the DNA from which the sequence was obtained. Such reference points can include the direction of transcription of other specified DNA sequences in the source DNA and/or the origin of replication of replicable vectors containing the sequence.

"Eukaryotic cell" refers to any mammalian or non-mammalian cell from a eukaryotic organism. By way of non-limiting example, any eukaryotic cell that is capable of being maintained under cell culture conditions and subsequently transfected would be included in this invention. Especially preferable cell types include, e. g., stem cells, embryonic stem cells, Chinese hamster ovary cells (CHO), COS, BHK21, NIH3T3, HeLa, C2C12, cancer cells, and primary differentiated or undifferentiated cells. Other suitable host cells are known to those skilled in the art.

The terms "host cell" and "recombinant host cell" are used interchangeably herein to indicate a eukaryotic cell into which one or more vectors of the invention have been introduced. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

The terms "introducing a purified DNA into a eukaryotic host cell" or "transfection" denote any process wherein an extracellular DNA, with or without accompanying material, enters a host cell. The term "cell transfected" or "transfected cell" means the cell into which the extracellular DNA has been introduced and thus harbours the extracellular DNA. The DNA might be introduced into the cell so that the nucleic acid is replicable either as a chromosomal integrant or as an extra chromosomal element.

"Promoter" as used herein refers to a nucleic acid sequence that regulates expression of a gene.

"Co-transfection" means the process of transfecting a eukaryotic cell with more than one exogenous gene, or vector, or plasmid, foreign to the cell, one of which may confer a selectable phenotype on the cell.

The purified and isolated DNA sequence having protein production increasing activity also comprises, besides one or more bent DNA element, at least one binding site for a DNA binding protein.

Usually the DNA binding protein is a transcription factor. Examples of transcription factors are the group comprising the polyQpolyP domain proteins.
Another example of a transcription factor is a transcription factor selected from the group comprising SATB1, NMP4, MEF2, S8, DLX1, FREAC7, BRN2, GATA 1/3, TATA, Bright, MSX, AP1, C/EBP, CREBP1, FOX, Freac7, HFH1, HNF3alpha, Nkx25, POU3F2, Pit1, TTF1, XFD1, AR, C/EBPgamma, Cdc5, FOXD3, HFH3, HNF3 beta, MRF2, Oct1, POU6F1, SRF, V$MTATA_B, XFD2, Bach2, CDP CR3, Cdx2, FOXJ2, HFL, HP1, Myc, PBX, Pax3, TEF, VBP, XFD3, Brn2, COMP1, Evil, FOXP3, GATA4, HFN1, Lhx3, NKX3A, POU1F1, Pax6, TFIIA or a combination of two or more of these transcription factors are preferred. Most preferred are SATB1, NMP4, MEF2 and polyQpolyP domain proteins.

SATB1, NMP4 and MEF2, for example, are known to regulate the development and/or tissue-specific gene expression in mammals. These transcription factors have the capacity to alter DNA geometry, and reciprocally, binding to DNA as an allosteric ligand modifies their structure. Recently, SATB1 was found to form a cage-like structure circumscribing heterochromatin (Cai S, Han HJ , and Kohwi-Shigematsu T, "Tissue-specific nuclear architecture and gene expression regulated by SATB1" *Nat Genet*, 2003. 34(1): p. 42-51).

Yet another object of the present invention is to provide a purified and isolated cLysMAR element and/or fragment, a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.

More preferably, the cLysMAR element and/or fragment are consisting of at least one nucleotide sequence selected from the B, K and F regions.

A further object of the present invention is to provide a synthetic MAR sequence comprising natural MAR element and/or fragments assembled between linker sequences.

Preferably, the synthetic MAR sequence comprises a cLysMAR element and/or fragment a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants. Also preferably, linker sequences are BglII-BamHI linker.

An other aspect of the invention is to provide a method for identifying a MAR sequence using a Bioinformatic tool comprising the computing of values of one or more DNA sequence features corresponding to DNA bending, major groove depth and minor groove width potentials and melting temperature. Preferably, the identification of one or more DNA sequence features further comprises a further DNA sequence feature corresponding to binding sites for DNA binding proteins, which is also computed with this method.

Preferably, profiles or weight-matrices of said bioinformatic tool are based on dinucleotide recognition.

The bioinformatic tool used for the present method is preferably, SMAR Scan®, which contains algorithms developed by Gene Express (http://srs6.bionet.nsc.ru/srs6bin/cgi-bin/wgetz?-e+[FEATURES-SiteID:'nR']) and based on Levitsky *et al.*, 1999. These algorithms recognise profiles, based on dinucleotides weight-matrices, to compute the theoretical values for conformational and physicochemical properties of DNA.

Preferably, SMAR Scan® uses the four theoretical criteria also designated as DNA sequence features corresponding to DNA bending, major groove depth and minor groove width potentials, melting temperature in all possible combination, using scanning windows of variable size (see Fig. 3). For each function used, a cut-off value has to be set. The program returns a hit every time the computed score of a given region is above the set cut-off value for all of the chosen criteria. Two data output modes are available to handle the hits, the first (called "profile-like") simply returns all hit positions on the query sequence and their corresponding values for the different criteria chosen. The second mode (called "contiguous hits ") returns only the positions of several contiguous hits and their corresponding sequence. For this mode, the minimum number of contiguous hits is another cut-off value that can be set, again with a tunable window size. This second mode is the default mode of SMAR Scan®. Indeed, from a semantic point of view, a hit is considered as a core-unwinding element (CUE), and a cluster of CUEs accompanied by clusters of binding sites for relevant proteins is considered as a MAR. Thus, SMAR Scan® considers only several contiguous hits as a potential MAR.

To tune the default cut-off values for the four theoretical structural criteria, experimentally validated MARs from SMARt DB (http://transfac.gbf.de/- SMARt DB) were used. All the human MAR sequences from the database were retrieved and analyzed with SMAR Scan® using the "profile-like" mode with the four criteria and with no set cut-off value. This allowed the setting of each function for every position of the sequences. The distribution for each criterion was then computed according to these data (see Fig. 1 and 3).

The default cut-off values of SMAR Scan® for the bend, the major groove depth and the minor groove width were set at the average of the 75th quantile and the median. For the melting temperature, the default cut-off value should be set at the 75th quantile. The minimum length for the "contiguous-hits" mode should be set to 300 because it is assumed to be the minimum length of a MAR (see Fig. 8 and 9). However, one skilled in the art would be able to determine the cut-off values for the above-mentioned criteria for a given organism with minimal experimentation.

Preferably, DNA bending values are comprised between 3 to 5 ° (radial degree). Most preferably they are situated between 3.8 to 4.4 °, corresponding to the smallest peak of Fig. 1.

Preferably the major groove depth values are comprised between 8.9 to 9.3 Å (Angström) and minor groove width values between 5.2 to 5.8 Å. Most preferably the major groove depth values are comprised between 9.0 to 9.2 Å and minor groove width values between 5.4 to 5.7 Å.

Preferably the melting temperature is comprised between 55 to 75 ° C (Celsius degree). Most preferably, the melting temperature is comprised between 55 to 62 ° C.

The DNA binding protein of which values can be computed by the method is usually a transcription factor preferably a polyQpolyP domain or a transcription factor selected

from the group comprising SATB1, NMP4, MEF2, S8, DLX1, FREAC7, BRN2, GATA 1/3, TATA, Bright, MSX, AP1, C/EBP, CREBP1, FOX, Freac7, HFH1, HNF3alpha, Nkx25, POU3F2, Pit1, TTF1, XFD1, AR, C/EBPgamma, Cdc5, FOXD3, HFH3, HNF3 beta, MRF2, Oct1, POU6F1, SRF, V$MTATA_B, XFD2, Bach2, CDP CR3, Cdx2, FOXJ2, HFL, HP1, Myc, PBX, Pax3, TEF, VBP, XFD3, Brn2, COMP1, Evil, FOXP3, GATA4, HFN1, Lhx3, NKX3A, POU1F1, Pax6, TFIIA or a combination of two or more of these transcription factors.

However, one skilled in the art would be able to determine other kinds of transcription factors in order to carry out the method according to the present invention.

In case SMAR Scan® is envisaged to perform, for example, large scale analysis, then, preferably, the above-mentioned method further comprises at least one filter predicting DNA binding sites for DNA transcription factors in order to reduce the computation.

The principle of this method combines SMAR Scan® to compute the structural features as described above and a filter, such as for example, the pfsearch, (from the pftools package as described in Bucher P, Karplus K, Moeri N, and Hofmann K, "A flexible search technique based on generalized profiles", *Computers and Chemistry* , 20:324, 1996) to predict the binding of some transcription factors.

Examples of filters comprise, but are not limited to, pfsearch, MatInspector, RMatch Professional and TRANSFAC Professional

This combined method uses the structural features of SMAR Scan® and the predicted binding of specific transcription factors of the filter that can be applied sequentially in any order to select MARs, therefore, depending on the filter is applied at the beginning or at the end of the method.

The first level selects sequences out of the primary input sequence and the second level, consisting in the filter, may be used to restrain among the selected sequences those which satisfy the criteria used by the filter.

In this combined method the filter detects clusters of DNA binding sites using profiles or weightmatrices from, for example, MatInspector (Quandt K, Frech K, Karas H, Wingender E, Werner T, "MatInd and MatInspector New fast and versatile tools for detection of consensus matches in nucleotide sequence data", *Nucleic Acids Research* , 23, 48784884, 1995.). The filter can also detect densities of clusters of DNA binding sites.

The combined method is actually a "wrapper" written in Perl for SMAR Scan® and, in case the pfsearch is used as a filter, from the pftools. The combined method performs a twolevel processing using at each level one of these tools (SMAR Scan® or filter) as a potential "filter", each filter being optional and possible to be used to compute the predicted features without doing any filtering.

If SMAR Scan® is used in the first level to filter subsequences, it has to be used with the "all the contiguous hits" mode in order to return sequences. If the pfsearch is used in the first level as first filter, it has to be used with only one profile and a distance in nucleotide needs to be provided. This distance is used to group together pfsearch hits that are located at a distance inferior to the distance provided in order to return sequences; The combined method launches pfsearch, parses its output and returns

sequences corresponding to pfsearch hits that are grouped together according to the distance provided. Then whatever the tool used in the first level, the length of the sub-sequences thus selected can be systematically extended at both ends according to a parameter called "hits extension".

The second and optional level can be used to filter out sequences (already filtered sequences or unfiltered input sequences) or to get the results of SMAR Scan® and/or pfsearch without doing any filtering on these sequences. If the second level of combined method is used to filter, for each criteria considered cutoff values (hit per nucleotide)need to be provided to filter out those sequences (see Fig. 20).

Another concern of the present invention is also to provide a method for identifying a MAR sequence comprising at least one filter detecting clusters of DNA binding sites using profiles or weightmatrices. Preferably, this method comprises two levels of filters and in this case, SMAR Scan® is totally absent from said method. Usually, the two levels consist in pfsearch.

Also embraced by the present invention is a purified and isolated MAR DNA sequence identifiable according to the method for identifying a MAR sequence using the described bioinformatic tool, the combined method or the method comprising at least one filter.
Analysis by the combined method of the whole human genome yielded a total of 1757 putative MARs representing a total of 1 065 305 base paires. In order to reduce the number of results, a dinucleotide analysis was performed on these 1757 MARs, computing each of the 16 possible dinucleotide percentage for each sequence considering both strands in the 5' to 3' direction.

Surprisingly, Applicants have shown that all of the "super" MARs detected with the combined method contain at least 10% of dinucleotide TA on a stretch of 100 contiguous base pairs. Preferably, these sequences contain at least 33% of dinucleotide TA on a stretch of 100 contiguous base pairs.

Applicants have also shown that these same sequences further contain at least 12% of dinucleotide AT on a stretch of 100 contiguous base pairs. Preferably, they contain at least 33% of dinucleotide AT on a stretch of 100 contiguous base pairs.

An other aspect of the invention is to provide a purified and isolated MAR DNA sequence of any of the preceding described MARs, comprising a sequence selected from the sequences SEQ ID Nos 1 to 27, a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.
Preferably, said purified and isolated MAR DNA sequence comprises a sequence selected from the sequences SEQ ID Nos 24 to 27, a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants. These sequences 24 to 27 correspond to those detected by the combined method and show a higher protein production increasing activity over sequences 1 to 23.

The present invention also encompasses the use of a purified and isolated DNA sequence comprising a first isolated matrix attachment region (MAR) nucleotide sequence which is a MAR nucleotide sequence selected from the group comprising

- a purified and isolated DNA sequence having protein production increasing activity,
- a purified and isolated MAR DNA sequence identifiable according to the method for identifying a MAR sequence using the described bioinformatic tool, the combined method or the method comprising at least one filter,
- the sequences SEQ ID Nos 1 to 27,
- a purified and isolated cLysMAR element and/or fragment,
- a synthetic MAR sequence comprising natural MAR element and/or fragments assembled between linker sequences,

a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants or a MAR nucleotide sequence of a cLysMAR element and/or fragment, a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants for increasing protein production activity in a eukaryotic host cell.

Said purified and isolated DNA sequence usually further comprises one or more regulatory sequences, as known in the art e.g. a promoter and/or an enhancer, polyadenylation sites and splice junctions usually employed for the expression of the protein or may optionally encode a selectable marker. Preferably said purified and isolated DNA sequence comprises a promoter which is operably linked to a gene of interest.

The DNA sequences of this invention can be isolated according to standard PCR protocols and methods well known in the art.

Promoters which can be used provided that such promoters are compatible with the host cell are, for example, promoters obtained from the genomes of viruses such as polyoma virus, adenovirus (such as Adenovirus 2), papilloma virus (such as bovine papilloma virus), avian sarcoma virus, cytomegalovirus (such as murine or human cytomegalovirus immediate early promoter), a retrovirus, hepatitis-B virus, and Simian Virus 40 (such as SV 40 early and late promoters) or promoters obtained from heterologous mammalian promoters, such as the actin promoter or an immunoglobulin promoter or heat shock promoters. Such regulatory sequences direct constitutive expression.

Furthermore, the purified and isolated DNA sequence might further comprise regulatory sequences which are capable of directing expression of the nucleic acid preferentially in a particular cell type (e. g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert,et al., 1987. Genes Dev.1: 268-277), lymphoid-specific promoters (Calame and Eaton, 1988. Adv. Immunol. 43: 235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989. EMBOJ. 8: 729-733) and immunoglobulins (Banerji, etal., 1983. Cell 33: 729-740; Queen and Baltimore, 1983. Cell 33:741-748), neuron-specific promoters (e. g., the neurofilament promoter;Byrne and Ruddle, 1989. Proc.Natl. Acad. Sci. USA 86: 5473-5477), pancreas-specific promoters (Edlund, et al., 1985. Science 230: 912-916), and mammary gland-specific promoters (e. g., milk whey promoter; U. S. Pat. No. 4,873,316 and European Application No. 264,166).

Developmentally-regulated promoters are also encompassed. Examples of such promoters include, e.g., the murine hox promoters (Kessel and Gruss, 1990. Science 249: 374-379) and thea-fetoprotein promoter (Campes and Tilghman, 1989. Genes

Dev. 3: 537-546).

Regulatable gene expression promoters are well known in the art, and include, by way of non-limiting example, any promoter that modulates expression of a gene encoding a desired protein by binding an exogenous molecule, such as the CRE/LOX system, the TET system, the doxycycline system, the NFkappaB/UV light system, the Leu3p/isopropylmalate system, and theGLVPc/GAL4 system (See e. g., Sauer, 1998, Methods 14 (4): 381-92 ; Lewandoski, 2001, Nat. Rev. Genet 2 (10): 743-55; Legrand-Poels et al., 1998, J. Photochem. Photobiol. B. 45: 18; Guo et al., 1996, FEBS Lett. 390 (2): 191-5; Wang et al., PNAS USA, 1999,96 (15): 84838).
However, one skilled in the art would be able to determine other kinds of promoters that are suitable in carrying out the present invention.

Enhancers can be optionally included in the purified DNA sequence of the invention then belonging to the regulatory sequence, e.g. the promoter.

The "gene of interest" or "transgene" preferably encodes a protein (structural or regulatory protein). As used herein "protein" refers generally to peptides and polypeptides having more than about ten amino acids. The proteins may be "homologous" to the host (i.e., endogenous to the host cell being utilized), or "heterologous," (i.e., foreign to the host cell being utilized), such as a human protein produced by yeast. The protein may be produced as an insoluble aggregate or as a soluble protein in the periplasmic space or cytoplasm of the cell, or in the extracellular medium. Examples of proteins include hormones such as growth hormone or erythropoietin (EPO), growth factors such as epidermal growth factor, analgesic substances like enkephalin, enzymes like chymotrypsin, receptors to hormones or growth factors, antibodies and include as well proteins usually used as a visualizing marker e.g. green fluorescent protein.

Preferably the purified DNA sequence further comprises at least a second isolated matrix attachment region (MAR) nucleotide sequence selected from the group comprising

- a purified and isolated DNA sequence having protein production increasing activity,
- a purified and isolated MAR DNA sequence identifiable according to the method for identifying a MAR sequence using the described bioinformatic tool, the combined method or the method comprising at least one filter,
- the sequences SEQ ID Nos 1 to 27,
- a purified and isolated cLysMAR element and/or fragment,
- a synthetic MAR sequence comprising natural MAR element and/or fragments assembled between linker sequences,

a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants. The isolated matrix attachment region (MAR) nucleotide sequence might be identical or different. Alternatively, a first and a second identical MAR nucleotide sequence are used.

Preferably, the MAR nucleotide sequences are located at both the 5' and the 3' ends of the sequence containing the promoter and the gene of interest. But the invention also envisions the fact that said first and or at least second MAR nucleotide sequences are located on a sequence distinct from the one containing the promoter and the gene of interest.

Embraced by the scope of the present invention is also the purified and isolated DNA sequence comprising a first isolated matrix attachment region (MAR) nucleotide sequence which is a MAR nucleotide sequence selected from the group comprising

- a purified and isolated DNA sequence having protein production increasing activity,
- a purified and isolated MAR DNA sequence identifiable according to the method for identifying a MAR sequence using the described bioinformatic tool, the combined method or the method comprising at least one filter,
- the sequences SEQ ID Nos 1 to 27,
- a purified and isolated cLysMAR element and/or fragment,
- a synthetic MAR sequence comprising natural MAR element and/or fragments assembled between linker sequences,

a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants that can be used for increasing protein production activity in a eukaryotic host cell by introducing the purified and isolated DNA sequence into a eukaryotic host cell according to well known protocols. Usually applied methods for introducing DNA into eukaryotic host cells applied are e.g. direct introduction of cloned DNA by microinjection or microparticle bombardment; electrotransfer ;use of viral vectors; encapsulation within a carrier system; and use of transfecting reagents such as calcium phosphate, diethylaminoethyl (DEAE) –dextran or commercial transfection systems like the Lipofect-AMINE 2000 (Invitrogen). Preferably, the transfection method used to introduce the purified DNA sequence into a eukaryotic host cell is the method for transfecting a eukaryotic cell as described below.

The purified and isolated DNA sequence can be used in the form of a circular vector. Preferably, the purified and isolated DNA sequence is used in the form of a linear DNA sequence as vector.

As used herein, "plasmid" and "vector" are used interchangeably, as the plasmid is the most commonly used vector form. However, the invention is intended to include such other forms of expression vectors, including, but not limited to, viral vectors (e. g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The present invention further encompasses a method for transfecting a eukaryotic host cell, said method comprising

a) introducing into said eukaryotic host cell at least one purified DNA sequence comprising at least one DNA sequence of interest and/or at least one purified and isolated DNA sequence comprising a MAR nucleotide sequence or other chromatin modifying elements,
b) subjecting within a defined time said transfected eukaryotic host cell to at least one additional transfection step with at least one purified DNA sequence comprising at least one DNA sequence of interest and/or with at least one purified and isolated DNA sequence comprising a MAR nucleotide sequence or other chromatin modifying elements
c) selecting said transfected eukaryotic host cell.

Preferably at least two up to four transfecting steps are applied in step b).

In order to select the successful transfected cells, a gene that encodes a selectable marker (e. g., resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. The gene that encodes a selectable marker might be located

on the purified DNA sequence comprising at least one DNA sequence of interest and/or at least one purified and isolated DNA sequence consisting of a MAR nucleotide sequence or other chromatin modifying elements or might optionally be co-introduced in separate form e.g. on a plasmid. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. The amount of the drug can be adapted as desired in order to increase productivity

Usually, one or more selectable markers are used. Preferably, the selectable markers used in each distinct transfection steps are different. This allows selecting the transformed cells that are "multi-transformed" by using for example two different antibiotic selections.

Any eukaryotic host cell capable of protein production and lacking a cell wall can be used in the methods of the invention. Examples of useful mammalian host cell lines include human cells such as human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol 36, 59 (1977)), human cervical carcinoma cells (HELA, ATCC CCL 2), human lung cells (W138, ATCC CCL 75), human liver cells (Hep G2, HB 8065); rodent cells such as baby hamster kidney cells (BHK, ATCC CCL 10), Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, *Proc. Natl. Acad. Sci. USA*, 77, 4216 (1980)), mouse sertoli cells (TM4, Mather, *Biol. Reprod* 23, 243-251 (1980)), mouse mammary tumor (MMT 060562, ATCC CCL51); and cells from other mammals such as monkey kidney CV1 line transformed by SV4O (COS-7, ATCC CRL 1651); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); myeloma (e.g. NS0) /hybridoma cells.
Preferably, the selected transfected eukaryotic host cells are high protein producer cells with a production rate of at least 10 pg per cell per day.
Most preferred for uses herein are mammalian cells, more preferred are CHO cells.

The DNA sequence of interest of the purified and isolated DNA sequence is usually a gene of interest preferably encoding a protein operably linked to a promoter as described above. The purified and isolated DNA sequence comprising at least one DNA sequence of interest might comprise additionally to the DNA sequence of interest MAR nucleotide sequence or other chromatin modifying elements.

Purified and isolated DNA sequence comprising a MAR nucleotide sequence are for example selected from the group comprising the sequences SEQ ID Nos 1 to 27 and/or particular elements of the cLysMAR e.g. the B, K and F regions as well as fragment and elements and combinations thereof as described above. Other chromatin modifying elements are for example boundary elements (BEs), locus control regions (LCRs), and universal chromatin opening elements (UCOEs) (see Zahn-Zabal et al. already cited). An example of multiple transfections of host cells is shown in Example 12 (Table 3). The first transfecting step (primary transfection) is carried out with the gene of interest (SV40EGFP) alone, with a MAR nucleotide sequence (MAR) alone or with the gene of interest and a MAR nucleotide sequence (MAR-SV40EGFP). The second transfecting step (secondary transfection) is carried out with the gene of interest (SV40EGFP) alone, with a MAR nucleotide sequence (MAR) alone or with the gene of interest and a MAR nucleotide sequence (MAR-SV40EGFP), in all possible combinations resulting from the first transfecting step.

Preferably the eukaryotic host cell is transfected by:

a) introducing a purified DNA sequence comprising one DNA sequence of interest and additionally a MAR nucleotide sequence,
b) subjecting within a defined time said transfected eukaryotic host cell to at least one additional transfection step with the same purified DNA sequence comprising one DNA sequence of interest and additionally a MAR nucleotide sequence of step a).

Also preferably, the MAR nucleotide sequence of the of the purified and isolated DNA sequence is selected form the group comprising

- a purified and isolated DNA sequence having protein production increasing activity,
- a purified and isolated MAR DNA sequence identifiable according to the method for identifying a MAR sequence using the described bioinformatic tool, the combined method or the method comprising at least one filter,
- the sequences SEQ ID Nos 1 to 27,
- a purified and isolated cLysMAR element and/or fragment,
- a synthetic MAR sequence comprising natural MAR element and/or fragments assembled between linker sequences,

a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.

Surprisingly, a synergy between the first and second transfection has been observed. A particular synergy has been observed when MAR elements are present at one or both of the transfection steps. Multiple transfections of the cells with pMAR alone or in combination with various expression plasmids, using the method described above have been carried out. For example, Table 3 shows that transfecting the cells twice with the pMAR-SV40EGFP plasmid gave the highest expression of GFP and the highest degree of enhancement of all conditions (4.3 fold). In contrast, transfecting twice the vector without MAR gave little or no enhancement, 2.8-fold, instead of the expected two-fold increase. This proves that the presence of MAR elements at each transfection step is of particular interest to achieve the maximal protein synthesis.
As a particular example of the transfection method, said purified DNA sequence comprising at least one DNA sequence of interest can be introduced in form of multiple unlinked plasmids, comprising a gene of interest operably linked to a promoter, a selectable marker gene, and/or protein production increasing elements such as MAR sequences.

The ratio of the first and subsequent DNA sequences may be adapted as required for the use of specific cell types, and is routine experimentation to one ordinary skilled in the art.

The defined time for additional transformations of the primary transformed cells is tightly dependent on the cell cycle and on its duration. Usually the defined time corresponds to intervals related to the cell division cycle.
Therefore this precise timing may be adapted as required for the use of specific cell types, and is routine experimentation to one ordinary skilled in the art.
Preferably the defined time is the moment the host cell just has entered into the same phase of a second or a further cell division cycle, preferably the second cycle.
This time is usually situated between 6h and 48 h, preferably between 20h and 24h after the previous transfecting event.

Also encompassed by the present invention is a method for transfecting a eukaryotic host cell, said method comprising co-transfecting into said eukaryotic host cell at least one first purified and isolated DNA sequence comprising at least one DNA sequence of

interest, and a second purified DNA comprising at least one MAR nucleotide selected from the group comprising:

- a purified and isolated DNA sequence having protein production increasing activity,
- a purified and isolated MAR DNA sequence identifiable according to the method for identifying a MAR sequence using the described bioinformatic tool, the combined method or the method comprising at least one filter,
- the sequences SEQ ID Nos 1 to 27,
- a purified and isolated cLysMAR element and/or fragment,
- a synthetic MAR sequence comprising natural MAR element and/or fragments assembled between linker sequences,

a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.
Said first purified and isolated DNA sequence can also comprise at least one MAR nucleotide as described above.
Also envisioned is a process for the production of a protein wherein a eukaryotic host cell is transfected according to the transfection methods as defined in the present invention and is cultured in a culture medium under conditions suitable for expression of the protein. Said protein is finally recovered according to any recovering process known to the skilled in the art.

Given as an example, the following process for protein production might be used. The eukaryotic host cell transfected with the transfection method of the present invention is used in a process for the production of a protein by culturing said cell under conditions suitable for expression of said protein and recovering said protein. Suitable culture conditions are those conventionally used for in vitro cultivation of eukaryotic cells as described e.g. in WO 96/39488. The protein can be isolated from the cell culture by conventional separation techniques such as e.g. fractionation on immunoaffinity or ion-exchange columns; precipitation; reverse phase HPLC; chromatography; chromatofocusing; SDS-PAGE; gel filtration. One skilled in the art will appreciate that purification methods suitable for the polypeptide of interest may require modification to account for changes in the character of the polypeptide upon expression in recombinant cell culture.

The proteins that are produced according to this invention can be tested for functionality by a variety of methods. For example, the presence of antigenic epitopes and ability of the proteins to bind ligands can be determined by Western blot assays, fluorescence cell sorting assays, immunoprecipitation, immunochemical assays and/or competitive binding assays, as well as any other assay which measures specific binding activity.

The proteins of this invention can be used in a number of practical applications including, but not limited to:
1. Immunization with recombinant host protein antigen as a viral/pathogen antagonist.
2. Production of membrane proteins for diagnostic or screening assays.
3. Production of membrane proteins for biochemical studies.
4. Production of membrane protein for structural studies.
5. Antigen production for generation of antibodies for immuno-histochemical mapping, including mapping of orphan receptors and ion channels.

Also provided by the present invention is a eukaryotic host cell transfected according to any of the preceding transfection methods. Preferably, the eukaryotic host cell is a mammalian host cell line.

As already described, example of useful mammalian host cell lines include human cells such as human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol 36, 59 (1977)), human cervical carcinoma cells (HELA, ATCC CCL 2), human lung cells (W138, ATCC CCL 75), human liver cells (Hep G2, HB 8065); rodent cells such as baby hamster kidney cells (BHK, ATCC CCL 10), Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, *Proc. Natl. Acad. Sci. USA*, 77, 4216 (1980)), mouse sertoli cells (TM4, Mather, *Biol. Reprod* 23, 243-251 (1980)), mouse mammary tumor (MMT 060562, ATCC CCL51); and cells from other mammals such as monkey kidney CV1 line transformed by SV4O (COS-7, ATCC CRL 1651); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL–1587); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); myeloma (e.g. NS0) /hybridoma cells.
Most preferred for uses herein are CHO cells.

The present invention also provides for a cell transfection mixture or Kit comprising at least one purified and isolated DNA sequence according to the invention.

The invention further comprises a transgenic organism wherein at least some of its cells have stably incorporated at least one DNA sequence of

- a purified and isolated DNA sequence having protein production increasing activity,
- a purified and isolated MAR DNA sequence identifiable according to the method for identifying a MAR sequence using the described bioinformatic tool, the combined method or the method comprising at least one filter,
- the sequences SEQ ID Nos 1 to 27,
- a purified and isolated cLysMAR element and/or fragment,
- a synthetic MAR sequence comprising natural MAR element and/or fragments assembled between linker sequences,

a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.
Preferably, some of the cells of the transgenic organisms have been transfected according the methods described herein.

Also envisioned in the present invention is a transgenic organism wherein its genome has stably incorporated at least one DNA sequence of

- a purified and isolated DNA sequence having protein production increasing activity,
- a purified and isolated MAR DNA sequence identifiable according to the method for identifying a MAR sequence using the described bioinformatic tool, the combined method or the method comprising at least one filter,
- the sequences SEQ ID Nos 1 to 27,
- a purified and isolated cLysMAR element and/or fragment,
- a synthetic MAR sequence comprising natural MAR element and/or fragments assembled between linker sequences,

a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.

Transgenic eukaryotic organisms which can be useful for the present invention are for example selected form the group comprising mammals (mouse, human, monkey etc) and in particular laboratory animals such as rodents in general, insects (drosophila,

etc), fishes (zebra fish, etc.), amphibians (frogs, newt, etc..) and other simpler organisms such as c. elegans, yeast, etc....

Yet another object of the present invention is to provide a computer readable medium comprising computer-executable instructions for performing the method for identifying a MAR sequence as described in the present invention.

The foregoing description will be more fully understood with reference to the following Examples. Such Examples, are, however, exemplary of methods of practising the present invention and are not intended to limit the scope of the invention.

EXAMPLES

Example 1: SMAR Scan® and MAR sequences

A first rough evaluation of SMAR Scan® was done by analyzing experimentally defined human MARs and non-MAR sequences. As MAR sequences, the previous results from the analysis of human MARs from SMARt Db were used to plot a density histogram for each criterion as shown in Fig. 1. Similarly, non-MAR sequences were also analyzed and plotted. As non-MAR sequences, all Ref-Seq-contigs from the chromosome 22 were used, considering that this latter was big enough to contain a negligible part of MAR sequences regarding the part of non-MAR sequences.

The density distributions shown in Fig. 1 are all skewed with a long tail. For the highest bend, the highest major groove depth and the highest minor groove width, the distributions are right skewed. For the lowest melting temperature, the distributions are left-skewed which is natural given the inverse correspondence of this criterion regarding the three others. For the MAR sequences, biphasic distributions with a second weak peak, are actually apparent. And between MAR and non-MAR sequences distributions, a clear shift is also visible in each plot.

Among all human MAR sequences used, in average only about 70% of them have a value greater than the 75th quantile of human MARs distribution, this for the four different criteria. Similarly concerning the second weak peak of each human MARs distribution, only 15% of the human MAR sequences are responsible of these outlying values. Among these 15% of human MAR sequences, most are very well documented MARs, used to insulate transgene from position effects, such as the interferon locus MAR, the beta-globin locus MAR (Ramezani A, Hawley TS, Hawley RG, "Performance- and safety-enhanced lentiviral vectors containing the human interferon-beta scaffold attachment region and the chicken beta-globin insulator", *Blood*, 101:4717-4724, 2003), or the apolipoprotein MAR (Namciu, S, Blochinger KB, Fournier REK, "Human matrix attachment regions in-sulate transgene expression from chromosomal position effects in Drosophila melanogaster", *Mol. Cell. Biol.*, 18:2382-2391, 1998).
Always with the same data, human MAR sequences were also used to determine the association between the four theoretical structural properties computed and the AT-content. Fig. 2 represents the scatterplot and the corresponding correlation coefficient r for every pair of criteria.

Example 2: Distribution plots of MAR sequences by organism

MAR sequences from SMARt DB of other organisms were also retrieved and analyzed similarly as explained previously. The MAR sequences density distributions for the mouse, the chicken, the sorghum bicolor and the human are plotted jointly in Fig. 3.

Example 3: MAR prediction of the whole chromosome 22

All RefSeq contigs from the chromosome 22 were analyzed by SMAR Scan® using the default settings this time. The result is that SMAR Scan® predicted a total of 803 MARs, their average length being 446 bp, which means an average of one MAR predicted per 42 777 bp. The total length of the predicted MARs corresponds to 1% of the chromosome 22 length. The AT-content of the predicted regions ranged from

65,1% to 93.3%; the average AT-content of all these regions being 73.5%. Thus, predicted MARs were AT-rich, whereas chromosome 22 is not AT-rich (52.1% AT).

SMARTest was also used to analyze the whole chromosome 22 and obtained 1387 MAR candidates, their average length being 494 bp representing an average of one MAR predicted per 24 765 bp. The total length of the predicted MARs corresponds to 2% of the chromosome 22. Between all MARs predicted by the two softwares, 154 predicted MARs are found by both programs, which represents respectively 19% and 11% of SMAR Scan® and SMARTest predicted MARs. Given predicted MARs mean length for SMAR Scan® and SMARTest, the probability to have by chance an overlapping between SMAR Scan® and SMARTest predictions is 0.0027% per prediction.

To evaluate the specificity of SMAR Scan® predictions, SMAR Scan® analyses were performed on randomly shuffled sequences of the chromosome 22 (Fig. 4). Shuffled sequences were generated using 4 different methods: by a segmentation of the chromosome 22 into nonoverlapping windows of 10 bp and by separately shuffling the nucleotides in each window; by "scrambling" which means a permutation of all nucleotides of the chromosome; by "rubbling" which means a segmentation of the chromosome in fragments of 10 bp and a random assembling of these fragments and finally by order 1 Markov chains, the different states being the all the different DNA dinucleotides and the transition probabilities between these states being based on the chromosome 22 scan. For each shuffling method, five shuffled chromosome 22 were generated and analyzed by SMAR Scan® using the default settings. Concerning the number hits, an average of 3 519 170 hits (sd: 18 353) was found for the permutated chromosome 22 within nonoverlapping windows of 10 bp, 171 936,4 hits (sd: 2 859,04) for the scrambled sequences and 24 708,2 hits (sd: 1 191,59) for the rubbled chromosome 22 and 2 282 hits in average (sd: 334,7) for the chromosomes generated according to order 1 Markov chains models of the chromosome 22, which respectively represents 185% (sd: 0.5% of the mean), 9% (sd: 1.5%), 1% (sd: 5%) and 0.1% (sd: 15%) of the number of hits found with the native chromosome 22. For the number of MARs predicted, which thus means contiguous hits of length greater than 300, 1 997 MARs were predicted with the shuffled chromosome 22 within windows of 10 bp (sd: 31.2), only 2.4 MARs candidates were found in scrambled sequences (sd: 0.96) and none for the rubbled and for the sequences generated according to Markov chains model, which respectively represents 249% and less than 0.3% of the number of predicted MARs found with the native chromosome 22. These data provide indications that SMAR Scan® detects specific DNA elements which organization is lost when the DNA sequences are shuffled .

Example 4: Analysis of known matrix attachment regions in the Interferon locus with SMAR Scan®

The relevance of MAR prediction by SMAR Scan® was investigated by analyzing the recently published MAR regions of the human interferon gene cluster on the short arm of chromosome 9 (9p22). Goetze et al. (already cited) reported an exhaustive analysis of the WP18A10A7 locus to analyze the suspected correlation between BURs (termed in this case stress-induced duplex destabilization or SIDD) and *in vitro* binding to the nuclear matrix (Fig. 9, lower part). Three of the SIDD peaks were in agreement with the *in vitro* binding assay, while others did not match matrix attachment sites. Inspection of the interferon locus with SMAR Scan® (Fig. 9, top part) indicated that three majors peaks accompanied by clusters of SATB1, NMP4 and MEF2 regulators binding sites

correlated well with the active MARs. Therefore, we conclude that the occurrence of predicted CUEs and binding sites for these transcription factors is not restricted to the *cLys*MAR but may be a general property of all MARs. These results also imply that the SMAR Scan® program efficiently detects MAR elements from genomic sequences.

Example 5: Accuracy of SMAR Scan® prediction and comparison with other predictive tools

The accuracy of SMAR Scan® was evaluated using six genomic sequences for which experimentally determined MARs have been mapped. In order to perform a comparison with other predictive tools, the sequences analyzed are the same with the sequences previously used to compare MAR-Finder and SMARTest. These genomic sequences are three plant and three human sequences (Table 1) totalizing 310 151 bp and 37 experimentally defined MARs. The results for SMARTest and MAR-Finder in Table 1 come from a previous comparison (Frisch M, Frech K, Klingenhoff A, Cartharius K, Liebich I and Werner T, In silico pre-diction of scaffold/matrix attachment regions in large genomic sequences, *Genome Researc*h, 12:349-354, 2001.).
MAR-Finder has been used with the default parameters excepted for the threshold that has been set to 0.4 and for the analysis of the protamine locus, the AT-richness rule has been excluded (to detect the non AT-rich MARs as was done for the protamine locus).

Sequence, description and reference	Length (kb)	Experimentally defined MARs positions (kb)	SMARTest prediction positions (kb)	MAR-Finder prediction positions (kb)	SMART Scan prediction positions (kb)
Oryza Sativa putative ADP-glucose pyrophosphorylase subunit SH2 and putative NADPH dependant reductase A1 genes (U70541). [4]	30.034	0.0-1.2 5.4-7.4 17.3-18.5 20.0-23.1	- **6.5-7.0** 15.2-15.7 16.2-16.6 **17.6-18.3** **19.6-20.1** **20.7-21.3** 23.6-23.9 25.0-25.4 27.5-27.9	- - 15.7-15.9 - **17.5-18.4** **19.8-20.4** **21.3-21.5** 23.9-24.2 24.7-25.1 -	- - 15.6-16 - **17.6-18.2** **21.6-22** - 23.4-23.8 - -
Sorghum bicolor ADP-glucose pyrophosphorylase subunit SH2, NADPH-dependant reducatse A1-b genes (AF010283). [4]	42.446	0.0-1.5 7.1-9.7 22.4-24.7 32.5-33.7 41.6-42.3	- - 21.3-21.9 **22.9-24.0** - 27.3-27.6 - -	- - - **23.2-24.2** - 26.9-27.5 - -	- **7.4-7.7** 21.5-21.8 **22.9-23.2** **23.6-24.0** 27.3-27.6 **33.4-33.9** -
Sorghum bicolor BAC clone 110K5 (AF124045). [37]	78.195	~0.9 ~5.8 ~6.3 ~9.3 ~15.0 ~18.5 ~21.9 ~23.3 ~25.6 ~29.1 ~34.6 ~44.1 ~48.5 ~57.9 ~62.9 ~67.1 ~69.3 ~73.7	- - - - 15.1-15.8 - **21.7-22.0** - - - - - **44.1-44.5** **47.9-49.5** - - **63.1-63.7** - - **74.3-74.7**	- - - - - - - - - - - - - **47.9-49.4** - - - - - -	- - - - - - **21.4-21.9** - - **29.2-29.5** - 39.0-40.0 - **48.1-48.6** **48.8-49.3** - - - - **74.3-74.6**
Human alpha-1-antitrypsin and corticosteroid binding globulin intergenic region (AF156545). [35]	30.461	2.6-6.3 22.0-30.4	**5.5-6.0** - **25.7-26.2** **27.5-27.8** - -	**3.0-3.2** **5.1-6.0** **24.9-25.3** **25.5-25.8** **26.2-26.4** **27.5-28.2**	**5.4-5.8** - **25.8-26.4** - -
Human protamine locus (U15422). [24]	53.060	8.8-9.7 32.6-33.6 37.2-39.4 51.8-53.0	- - - -	**8.0-8.9*** **33.9-34.8*** **33.9-34.8*** -*	- - - -
Human beta-globin locus (U01317). [21]	75.955	1.5-3.0 15.6-19.0 44.7-52.7 60.0-70.0	- **18.0-18.4** - 34.4-34.9 - 56.6-57.1 **59.8-60.3** **65.6-66.0**	- **15.5-16.0** **18.0-18.4** - **50.6-50.8** 56.5-57.2 **58.1-58.5** **63.0-63.6**	**2.3-2.6** **15.3-15.6** - - - - **62.8-63.1** -

			67.6-67.9 68.8-69.1	68.7-69.3 -	66.3-66.7 -
Sum(kb)	310.151	at least 56.1	14.5	13.8	9.5
Total numbers : Average kb /predicted MAR True positives [number of experimentally defined MAR found] False positives False negatives Specificity Sensitivity		37	28 11.076 19[14] 9 23 19/28= 68% 14/37= 38%	25 12.406 20[12] 5 25 20/25= 80% 12/37= 32%	22 14.097 17[14] 5 23 17/22= 77% 14/37= 38%

Table 1: Evaluation of SMAR Scan® accuracy

Six different genomic sequences, three plant and three human sequences, for which experimentally defined MARs are known, were analyzed with MAR-Finder, SMARTest and SMAR Scan®. True positive matches are printed in bold, minus (-) indicates false negative matches. Some of the longer experimentally defined MARs contained more than one in silico prediction, each of them was counted as true positive match. Therefore, the number of true in silico predictions is higher than the number of experimentally defined MARs found. Specificity is defined as the ratio of true positive predictions, whereas sensitivity is defined as the ratio of experimentally defined MARs found. * AT-rich rule excluded using MAR-Finder.

SMARTest predicted 28 regions as MARs, 19 (true positives) of these correlate with experimentally defined MARs (specificity: 68%) whereas 9 (32%) are located in non-MARs (false positives). As some of the longest experimentally determined MARs contains more than one in silico prediction, the 19 true positives correspond actually to 14 different experimentally defined MARs (sensitivity: 38%). MARFinder predicted 25 regions as MARs, 20 (specificity: 80%) of these correlate with experimentally defined MARs corresponding to 12 different experimentally defined MARs (sensitivity: 32%). SMAR Scan® predicted 22 regions, 17 being true positives (specificity: 77%) matching 14 different experimentally defined MARs (sensitivity: 38%).

As another example, the same analysis has been applied to human chromosomes 1 and 2 and lead to the determination of 23 MARs sequences (SEQ ID N° 1 to 23). These sequences are listed in Annex 1 in ST25 format.

Example 6: Analyses of the whole genome using the combined method (SMAR Scan®-pfsearch)

In order to test the potential correlation between the structural features computed by SMAR Scan® and the S/MAR functional activity, the whole human genome has been analyzed with the combined method with very stringent parameters, in order to get sequences with the highest values for the theoretical structural features computed, which are called "super" S/MARs below. This was done with the hope to obtain predicted MAR elements with a very potential to increase transgene expression and recombinant protein production. The putative S/MARs hence harvested were first analyzed from the bioinformatics perpective in an attempt to characterize and classify them.

6.1 S/MARs predicted from the analysis of the whole human genome

As whole human genome sequence, all human RefSeq (National Center for Biotechnology Information, The NCBI handbook [Internet]. Bethesda (MD): National Library of Medicine (US), Oct. Chapter 17, The Reference Sequence (RefSeq) Project, 2002 (Available from http://www.ncbi.nih.gov/entrez/query.fcgi?db=Books) contigs (release 5) were used and analyzed with the combined method, using SMAR Scan® as filter in the first level processing, employing default settings except for the highest bend cutoff value, whereas a stringent threshold of 4.0 degrees (instead of 3.202 degrees) has been used for the DNA bending criterion.

In the second level processing, predicted transcription factors binding have been sought in the sequences selected from the previous step without doing any filtering on these sequences.

The analysis by the combined method of the whole human genome came up with a total of 1757 putative "super" S/MARs representing a total of 1 065 305 bp (0.35% of the whole human genome). Table 2 shows for each chromosome: its size, its number of genes, its number of S/MARs predicted, its S/MARs density per gene and its kb per S/MAR. This table shows that there are very various gene densities per S/MAR predicted for the different chromosomes (standard deviation represents more than 50% of the mean of the density of genes per S/MAR predicted and the fold difference between the higher and the lower density of genes per S/MAR is 6,5). Table 2 also shows that the kb per S/MAR varies less that the density of genes per S/MAR (standard deviation represents 25% of the mean of kb per S/MAR and the fold difference between the higher and the lower kb per S/MAR is 3.2).

Chromosome	Number of genes per chromosome	Size of the chromosome (millions bp)	Number of S/MARs predicted	Density of genes per S/MAR	Kb per S/MAR
1	2544	230	85	29.9	2705
2	1772	241	143	12.3	1685
3	1406	198	101	13.9	1960
4	1036	190	118	8.7	1610
5	1233	180	116	10.6	1551
6	1247	170	94	13.2	1808
7	1383	160	179	7.7	1754
8	942	145	77	12.2	1883
9	1100	119	48	22.9	2479
10	1003	133	71	14.1	1873
11	1692	132	67	25.2	1970
12	1278	131	78	16.3	1679
13	506	97	70	7.2	1385
14	1168	88	36	32.4	2444
15	895	83	35	25.5	2371
16	1107	81	41	27	1975
17	1421	80	37	38.4	2162
18	396	75	51	7.7	1470
19	1621	56	36	45.02	1555
20	724	60	28	25.8	2142
21	355	34	18	19.7	1888
22	707	34	28	25.2	1214
X	1168	154	170	6.8	905
Y	251	25	30	8.3	833
Sum	26 955	3 050	1 757	457	433 12
Mean	1 123	127	73	19	1 804
Sd	510	72.8	45	10	462

Table 2: Number of S/MARs predicted per chromosome. The number of genes per chromosome

corresponds to the NCBI human genome statistics (Build 34 Version 3) (National Center for Biotechnology Information, The NCBI handbook [Internet]. Bethesda (MD): National Library of Medicine (US), Oct. Chapter 17, The Reference Sequence (RefSeq) Project, 2002 (Available from http://www.ncbi.nih.gov/entrez/query.fcgi?db=Books) based on GenBank annotations. Chromosome sizes are the sum of the corresponding human RefSeq (National Center for Biotechnology Information, The NCBI handbook [Internet]. Bethesda (MD): National Library of Medicine (US), Oct. Chapter 17, The Reference Sequence (RefSeq) Project, 2002 (Available from http://www.ncbi.nih.gov/entrez/query.fcgi?db=Books) (release 5) contig lengths

6.2 Bioinformatics analysis of "super" MARS for transcription factor binding sites

The 1757 predicted "super" S/MARs sequences obtained previously by SMAR Scan® were then analyzed for potential transcription factors binding sites. This has been achieved using RMatch™ Professional (Kel AE, Gossling E, Reuter I, Cheremushkin E, KelMargoulis OV, Wingender E, MATCH: A tool for searching transcription factor binding sites in DNA sequences, *Nucleic Acids Res.* 31(13):35769, 2003), a weight matrixbased tool based on TRANSFAC (Wingender E, Chen X, Fricke E, Geffers R, Hehl R, Liebich I, Krull M, Matys V, Michael H, Ohnhauser R, Pruss M, Schacherer F, Thiele S, Urbach S, The TRANSFAC system on gene expression regulation, *Nucleic Acids Research* , 29(1):2813, 2001). Match™ 2.0 Professional has been used with most of the default settings Match™ analysis was based on TRANSFAC Professional, release 8.2 (20040630). The sums of all transcription factors binding prediction on the 1757 sequences analyzed according to Match™ are in Table 3. Based on this table, only the transcription factors totalizing at least 20 hits over the 1757 sequences analyzed were considered for further analyses.

Hereafter are some of the human transcription factors that are the most often predicted to bind on the 1757 putative S/MAR sequences and their Match description: Cdc5 (cell division control protein 5) a transcriptional regulator/repressor, Nkx3A a homeodomain protein regulated by androgen, POU1F1 (pituitaryspecific positive transcription factor 1) which is specific to the pituitary and stimulates cells proliferation. Thus, in addition to SATB1, NMP4 and MEF2, other transcription factors can participate in the activity of MARs.

AP1	1	AR	2	Bach2	1	Brn2	1
C/EBP	20	C/EBPgamma	5	CDP CR3	1	COMP1	2
CREBP1	34	Cdc5	858	Cdx2	35	Evi1	472
FOX	78	FOXD3	79	FOXJ2	244	FOXP3	29
Freac7	272	GATA1	2	GATA3	142	GATA4	125
HFH1	12	HFH3	1	HLF	275	HNF1	337
HNF3alpha	23	HNF3beta	71	HP1	2	Lhx3	22
MEF2	114	MRF2	57	Myc	18	NKX3A	849
Nkx25	2	Oct1	191	PBX	5	POU1F1	483
POU3F2	11	POU6F1	29	Pax3	3	Pax6	20
Pit1	505	SRF	8	TEF	2852	TFIIA	14
TTF1	1	V$MTATA_B	4	VBP	53	Vmw65	1
XFD1	65	XFD2	418	XFD3	2		

Table 3 is a summary of all transcription factors binding prediction (totalizing 20 hits or more) on the 1757 sequences analyzed.

6.3 Bioinformatics analysis of predicted "super" MARs for dinucleotide frequencies

Various computer analysis were performed in order to easily identify "super" S/MAR sequences using an explicit criterion that could be identified without computing. Among those, a di-nucleotide analysis was performed on the 1757 superMARs, computing each of the 16 possible dinucleotide percentage for each sequence considering both strands in the 5' > 3' direction.

A summary (min., max., median, mean, 25th percentile and 75th percentile) as well as the histograms of each dinucleotide percentage over the 1757 S/MAR sequences are respectively presented in Table 4. A similar analysis was performed on randomly selected sequences from the human genome, representing randomly selected non-S/MAR sequences (which might however contain some MARs). Table 5 represents respectively a summary of the dinucleotide content analysis for these sequences.

Table 4: Dinucleotide percentages over the 1757 S/MAR sequences

	AA %	AC %	AG %	AT %
Minimum	0.000	0.0000	0.0000	18.50
25th percentile	4.234	0.9372	0.1408	32.11
Median	7.843	2.2408	0.4777	34.68
Mean	7.184	3.2117	1.0865	34.32
75th percentile	10.110	4.7718	1.5096	36.94
Maximum	17.290	12.9479	8.1230	50.00
	CA %	CC %	CG %	CT %
Minimum	0.0000	0.00000	0.0000	0.0000
25th percentile	0.9695	0.00000	0.0000	0.1408
Median	1.9776	0.00000	0.0000	0.4777
Mean	2.6977	0.14123	0.2709	1.0865
75th percentile	3.7543	0.09422	0.1256	1.5096
Maximum	10.4061	4.24837	7.4410	8.1230
	GA %	GC %	GG %	GT %
Minimum	0.00000	0.0000	0.00000	0.0000
25th percentile	0.08696	0.0000	0.00000	0.9372
Median	0.32616	0.0000	0.00000	2.2408
Mean	0.63347	0.2104	0.14123	3.2117
75th percentile	0.83333	0.1914	0.09422	4.7718
Maximum	5.77889	9.8795	4.24837	12.9479
	TA %	TC %	TG %	TT %
Minimum	28.63	0.00000	0.0000	0.000
25th percentile	33.48	0.08696	0.9695	4.234
Median	35.22	0.32616	1.9776	7.843
Mean	35.29	0.63347	2.6977	7.184
75th percentile	37.14	0.83333	3.7543	10.110
Maximum	50.00	5.77889	10.4061	17.290

Considering the results of the predicted S/MAR elements and of the nonS/MAR sequences in the summary tables, noticeable differences can be noticed in the AT et TA dinucleotide contents between these two groups of sequences. AT and TA represent respectively at least 18,5 % and 28.6 % of the dinucleotide content of the predicted S/MAR sequences, whereas the minimum percentages for the same dinucleotides in

nonS/MAR sequences are respectively 0.3 % and 0%. Similarly, the maximum CC and GG content in S/MAR sequences is 4.2 %, whereas in nonS/MAR sequences the percentages for these two dinucleotides can amount up to 20.8 %.

The correlation between AT and TA dinucleotide percentages and the DNA highest bend as computed by SMAR Scan® is depicted in Fig. 17 for the predicted S/MAR sequences and in Fig.18 for the nonS/MAR sequences. The different scatterplots of these figures show that the TA percentage correlates well with the predicted DNA bend as predicted by SMAR Scan®.

Table 5: Dinucleotide percentages over the 1757 nonS/MAR sequences summary

	AA %	AC %	AG %	AT %
Minimum	0.000	1.735	1.512	0.3257
25th percentile	7.096	4.586	6.466	5.1033
Median	9.106	5.016	7.279	6.8695
Mean	8.976	5.054	7.184	7.0108
75th percentile	10.939	5.494	7.969	8.7913
Maximum	17.922	13.816	12.232	23.1788
	CA %	CC %	CG %	CT %
Minimum	3.571	0.8278	0.0000	1.512
25th percentile	6.765	4.1077	0.4727	6.466
Median	7.410	5.5556	0.8439	7.279
Mean	7.411	5.9088	1.2707	7.184
75th percentile	8.010	7.2460	1.5760	7.969
Maximum	15.714	20.8415	12.6074	12.232
	GA %	GC %	GG %	GT %
Minimum	1.319	0.4967	0.8278	1.735
25th percentile	5.495	3.2615	4.1077	4.586
Median	6.032	4.4092	5.5556	5.016
Mean	6.065	4.7468	5.9088	5.054
75th percentile	6.602	5.8824	7.2460	5.494
Maximum	10.423	16.0000	20.8415	13.816
	TA %	TC %	TG %	TT %
Minimum	0.000	1.319	3.571	0.000
25th percentile	3.876	5.495	6.765	7.096
Median	5.625	6.032	7.410	9.106
Mean	5.774	6.065	7.411	8.976
75th percentile	7.464	6.602	8.010	10.939
Maximum	24.338	10.423	15.714	17.922

Four of the novel super MARs were randomly picked and analyzed for AT and TA dinucleotide content, and compared with the previously known chicken lysMAR, considering windows of 100 base pairs (Table 6).

Surprinsigly, Applicants have shown that all of the super MARs have AT dinucleotide frequencies greater then 12%, and TA dinucleotides greater than 10% of the total dinucleotides analysed in a window of 100base pairs of DNA. The most efficient MARs display values around 34% of the two dinucleotide pairs.

Table 6. Summary of %AT and TA dinucleotide frequencies of experimentally verified MARs

CLysMAR (average of CUEs)	AT% : 12.03	TA% : 10.29	SEQ ID No
P1_68	AT% : 33.78	TA% : 33.93	SEQ ID No
P1_6	AT% : 34.67	TA% : 34.38	SEQ ID No

P1_42	AT% : 35.65	TA% : 35.52	SEQ ID No
Mean value for all human "super"MARs	AT% : 34.32	TA% : 35.29	
Mean value for all human non-MARs	AT% : 7.01	TA% : 5.77	

6.4 Analysis of orthologous intergenic regions of human and mouse genomes

In order to get an insight on S/MAR evolution, orthologous intergenic regions of human and mouse genomes have been analysed with SMAR Scan®. The data set used is composed of 87 pairs of complete orthologous intergenic regions from the human and mouse genomes (Shabalina SA, Ogurtsov AY, Kondrashov VA, Kondrashov AS, Selective constraint in intergenic regions of human and mouse genomes, *Trends Genet*, 17(7):3736, 2001) (average length ~12 000 bp) located on 12 human and on 12 mouse chromosomes, the synteny of these sequences was confirmed by pairwise sequence alignment and consideration of the annotations of the flanking genes (experimental or predicted).

Analysis of the 87 human and mouse orthologous intergenic sequences have been analysed with SMAR Scan® using its default settings. Analysis of the human sequences yielded a total of 12 S/MARs predicted (representing a total length of 4 750 bp), located on 5 different intergenic sequences.

Among the three human intergenic sequences predicted to contain a "super" S/MAR using SMAR Scan® stringent settings, one of the corresponding mouse orthologous intergenic sequence is also predicted to contain a S/MAR (human EMBL ID: Z96050, position 28 010 to 76 951 othologous to mouse EMBL ID: AC015932, positions 59 884 to 89 963). When a local alignement of these two orthologous intergenic sequences is performed, the best local alignement of these two big regions correspond to the regions predicted by SMAR Scan® to be S/MAR element. A manual search for the mouse orthologs of the two other human intergenic sequences predicted to contain a "super" S/MAR was performed using the Ensembl Genome Browser (http://ensembl.org). The mouse orthologous intergenic sequences of these two human sequences were retrieved using Ensembl orthologue predictions (based on gene names), searching the orthologous mouse genes for the pairs of human genes flanking these intergenic regions.

Because SMAR Scan® has been tuned for human sequences and consequently yields little "super"MARs with mouse genomic sequences, its default cutoff values were slightly relaxed for the minimum size of contiguous hits to be considered as S/MAR (using 200 bp instead of 300 bp). Analysis by SMAR Scan® of these mouse sequences predicted several S/MARs having high values for the different computed structural features. This finding suggests that the human MAR elements are conserved across species.

Example 7 : Dissection of the chicken lysozyme gene 5'- MAR

The 3000 base pair 5'-MAR was dissected into smaller fragments that were monitored for effect on transgene expression in Chinese hamster ovary (CHO) cells. To do so, seven fragments of ~400 bp were generated by polymerase chain reaction (PCR). These PCR-amplified fragments were contiguous and cover the entire MAR sequence when placed end-to-end. Four copies of each of these fragments were ligated in a head-to-tail orientation, to obtain a length corresponding to approximately half of that of

the natural MAR. The tetramers were inserted upstream of the SV40 promoter in pGEGFPControl, a modified version of the pGL3Control vector (Promega). The plasmid pGEGFPControl was created by exchanging the luciferase gene of pGL3Control for the EGFP gene from pEGFP-N1 (Clontech). The 5'-MAR-fragment-containing plasmids thus created were co-transfected with the resistance plasmid pSVneo in CHO-DG44 cells using LipofectAmine 2000 (Invitrogen) as transfection reagent, as performed previously (Zahn-Zabal, M., et al., "Development of stable cell lines for production or regulated expression using matrix attachment regions" *J Biotechnol*, 2001. 87(1): p. 29-42.). After selection of the antibiotic (G-418) resistant cells, polyclonal cell populations were analyzed by FACS for EGFP fluorescence.

Transgene expression was expressed at the percentile of high expressor cells, defined as the cells which fluorescence levels are at least 4 orders of magnitude higher than the average fluorescence of cells transfected with the pGEGFPControl vector without MAR. Fig. 5 shows that multimerized fragments B, K and F enhance transgene expression, despite their shorter size as compared to the original MAR sequence. In contrast, other fragments are poorly active or fully inactive.

Example 8 : Specificity of B, K and F regions in the MAR context

The 5'-MAR was serially deleted from the 5'-end (Fig.6, upper part) or the 3'-end (Fig.6, lower part), respectively. The effect of the truncated elements was monitored in an assay similar to that described in the previous section. Figure 6 shows that the loss of ability to stimulate transgene expression in CHO cells was not evenly distributed.

In this deletion study, the loss of MAR activity coincided with discrete regions of transition which overlap with the 5'-MAR B-, K- and F-fragment, respectively. In 5' deletions, activity was mostly lost when fragment K and F were removed. 3' deletions that removed the F and b elements had the most pronounced effects. In contrast, flanking regions A, D, E and G that have little or no ability to stimulate transgene expression on their own (Fig. 5), correspondingly did not contribute to the MAR activity in the 5'- and 3'-end deletion studies (Fig. 6).

Example 9:Structure of the F element

The 465 bp F fragment was further dissected into smaller sub-fragments of 234, 243, 213 bp and 122, 125 and 121 bp, respectively. Fragments of the former group were octamerized (8 copies) in a head-to-tail orientation, while those of the latter group were similarly hexa-decamerized (16 copies), to maintain a constant length of MAR sequence. These elements were cloned in pGEGFPControl vector and their effects were assayed in CHO cells as described previously. Interestingly, fragment FIII retained most of the activity of the full-length F fragment whereas fragment FII, which contains the right-hand side part of fragment FIII, lost all the ability to stimulate transgene expression (Fig. 7). This points to an active region comprised between nt 132 and nt 221 in the FIB fragment. Consistently, multiple copies of fragments FI and FIB, which encompass this region, displayed similar activity. FIIA on its own has no activity. However, when added to FIB, resulting in FIII, it enhances the activity of the former. Therefore FIIA appears to contain an auxiliary sequence that has little activity on its own, but that strengthens the activity of the minimal domain located in FIB.

Analysis of the distribution of individual motifs within the lysozyme gene 5'-MAR is shown in Fig. 8 A, along with some additional motifs that we added to the analysis. Most of these motifs were found to be dispersed throughout the MAR element, and not

specifically associated with the active portions. For instance, the binding sites of transcription factors and other motifs that have been associated with MARs were not preferentially localized in the active regions. It has also been proposed that active MAR sequences may consist of combination of distinct motifs. Several computer programs (MAR Finder, SMARTest, SIDD duplex stability) have been reported to identify MARs as regions of DNA that associate with the DNA matrix. They are usually based on algorithms that utilizes a predefined series of sequence-specific patterns that have previously been suggested as containing MAR activity, as exemplified by MAR Finder, now known as MAR Wiz. The output of these programs did not correlate well with the transcriptionally active portions of the *cLysMAR*. For instance, peaks of activity obtained with MAR Finder did not clearly match active MAR sub-portion, as for instance the B fragment is quite active in vivo but scores negative with MAR Finder (Fig. 8B, compare the top and middle panels). Bent DNA structures, as predicted by this program, did not correlate well either with activity (Fig. 8B, compare the top and bottom panels). Similar results were obtained with the other available programs (data not shown).

The motifs identified by available MAR prediction computer methods are therefore unlikely to be the main determinants of the ability of the *cLysMAR* to increase gene expression. Therefore, a number of other computer tools were tested. Surprisingly, predicted nucleosome binding sequences and nucleosome disfavouring sequences were found to be arranged in repetitively interspersed clusters over the MAR, with the nucleosome favouring sites overlapping the active B, K and F regions. Nucleosome positioning sequences were proposed to consist of DNA stretches that can easily wrap around the nucleosomal histones, and they had not been previously associated with MAR sequences.

Nucleosome-favouring sequences may be modelled by a collection of DNA features that include moderately repeated sequences and other physico-chemical parameters that may allow the correct phasing and orientation of the DNA over the curved histone surface. Identification of many of these DNA properties may be computerized, and up to 38 different such properties have been used to predict potential nucleosome positions. Therefore, we set up to determine if specific components of nucleosome prediction programs might correlate with MAR activity, with the objective to construct a tool allowing the identification of novel and possibly more potent MARs from genomic sequences.

To determine whether any aspects of DNA primary sequence might distinguish the active B, K and F regions from the surrounding MAR sequence, we analyzed the 5'-MAR with MAR Scan®. Of the 38 nucleosomal array prediction tools, three were found to correlate with the location of the active MAR sub-domains (Fig. 9A). Location of the MAR B, K and F regions coincides with maxima for DNA bending, major groove depth and minor groove width. A weaker correlation was also noted with minima of the DNA melting temperature, as determined by the GC content. Refined mapping over the MAR F fragment indicated that the melting temperature valley and DNA bending summit indeed correspond the FIB sub-fragment that contains the MAR minimal domain (Fig. 9B). Thus active MAR portions may correspond to regions predicted as curved DNA regions by this program, and we will refer to these regions as CUE-B, CUE-K and CUE-F in the text below. Nevertheless, whether these regions correspond to actual bent DNA and base-pair unwinding regions is unknown, as they do not correspond to bent DNA as predicted by MAR Wiz (Fig.9B).

Example 10 : Imprints of other regulatory elements in the F fragment

Nucleosome positioning features may be considered as one of the many specific chromatin codes contained in genomic DNA. Although this particular code may contribute to the activity of the F region, it is unlikely to determine MAR activity alone, as the 3' part of the F region enhanced activity of the minimal MAR domain contained in the FIB portion. Using the MatInspector program (Genomatix), we searched for transcription factor binding sites with scores higher than 0.92 and found DNA binding sequences for the NMP4 and MEF2 proteins in the 3' part of the F fragment (Fig. 8B). To determine whether any of these transcription factor-binding sites might localize close to the B and K active regions, the entire 5'-MAR sequence was analyzed for binding by NMP4 and MEF2 and proteins reported to bind to single-stranded or double-stranded form of BURs. Among those, SATB1 (special AT-rich binding protein 1) belongs to a class of DNA-binding transcription factor that can either activate or repress the expression of nearby genes. This study indicated that specific proteins such as SATB1, NMP4 (nuclear matrix protein 4) and MEF2 (myogenic enhancer factor 2), have a specific distribution and form a framework around the minimal MAR domains of *cLysMAR* (Fig. 10). The occurrence of several of these NMP4 and SATB1 binding sites has been confirmed experimentally by the EMSA analysis of purified recombinant proteins (data not shown).

Example 11 : Construction of artificial MARs by combining defined genetic elements

To further assess the relative roles of the various MAR components, the *cLysMAR* was deleted of all three CUE regions (Fig. 11, middle part), which resulted in the loss of part of its activity when compared to the complete MAR sequence similarly assembled from all of its components as a control (Fig. 11, top part). Consistently, one copy of each CUE alone, or one copy of each of the three CUEs assembled head-to-tail, had little activity in the absence of the flanking sequences. These results strengthen the conclusion that optimal transcriptional activity requires the combination of CUEs with of flanking sequences. Interestingly, the complete MAR sequence generated from each of its components, but containing also BglII-BamHI linker sequences (AGATCC) used to assemble each DNA fragment, displayed high transcriptional activity (6 fold activation) as compared to the 4.8 fold noted for the original MAR element in this series of assays (see Fig. 5).

We next investigated whether the potentially curved DNA regions may also be active in an environment different from that found in their natural MAR context. Therefore, we set up to swap the CUE-F, CUE-B and CUE-K elements, keeping the flanking sequences unchanged. The sequences flanking the CUE-F element were amplified by PCR and assembled to bracket the various CUEs, keeping their original orientation and distance, or without a CUE. These engineered ~1.8 kb MARs were then assayed for their ability to enhance transgene expression as above. All three CUE were active in this context, and therefore there action is not restricted to one given set of flanking sequences. Interestingly, the CUE-K element was even more active than CUE-F when inserted between the CUE-F flanking sequences, and the former composite construct exhibited an activity as high as that observed for the complete natural MAR (4.8 fold activation). What distinguishes the CUE-K element from CUE-F and CUE-B is the presence of overlapping binding sites for the MEF-2 and SatB1 proteins, in addition to its CUE feature. Therefore, fusing CUE-B with CUE-F-flanking domain results in a higher density of all three binding sites, which is likely explanation to the increased activity. These results indicate that assemblies of CUEs with sequences containing binding sites

for proteins such as NMP4, MEF-2, SatB1, and/or polyPpolyQ proteins constitute potent artificial MAR sequences.

Example 12 : Expression vectors

Three expression vectors according to the present invention are represented on Figure 12.

Plasmid pPAG01 is a 5640 bp pUC19 derivative. It contains a 2960 bp chicken DNA fragment cloned in *BamH1* and *Xbal* restriction sites. The insert comes from the border of the 5'-end of the chicken lyzozyme locus and has a high A/T-content.

Plasmid pGEGFP (also named pSV40EGFP) control is a derivative of the pGL3-control vector (Promega) in which the luciferase gene sequence has been replaced by the EGFP gene sequence form the pEGFP-N1 vector (Clontech). The size of pGEGFP plasmid is 4334bp.

Plasmid pUbCEGFP control is a derivative of the pGL3 wit an Ubiquitin promoter.

Plasmid pPAG01GFP (also named pMAR-SV40EGFP) is a derivative of pGEGFP with the 5'-Lys MAR element cloned in the MCS located just upstream of the SV40 promoter. The size of the pPAG01EGF plasmid is 7285bp.

Example 13 ; Effect of the additional transfection of primary transfectant cells on transgene expression

One day before transfection, cells were plated in a 24-well plate, in growth medium at a density of 1.35 x 10^5 cells/well for CHO-DG44 cells. 16 hours post-inoculum, cells were transfected when they reached 30-40% confluence, using Lipofect-AMINE 2000 (hereinafter LF2000), according to the manufacturer's instructions (Invitrogen). Twenty-seven microliters of serum free medium (Opti-MEM; Invitrogen) containing 1.4 µl of LF2000 were mixed with 27 µl of Opti-MEM containing 830 ng of linear plasmid DNA. The antibiotic selection plasmid (pSVneo) amounted to one tenth of the reporter plasmid bearing the GFP transgene. The mix was incubated at room temperature for 20 min, to allow the DNA-LF2000 complexes to form. The mixture was diluted with 300 µl of Opti-MEM and poured into previously emptied cell-containing wells. Following 3 hours incubation of the cells with the DNA mix at 37°C in a CO_2 incubator, one ml of DMEM-based medium was added to each well. The cells were further incubated for 24 hours in a CO_2 incubator at 37°C. The cells were then transfected a second time according to the method described above, except that the resistance plasmid carried another resistance gene (pSVpuro). Twenty-four hours after the second transfection, cells were passaged and expanded into a T-75 flask containing selection medium supplemented with 500 µg/ml G-418 and 5 µg/ml puromycin. After a two week selection period, stably transfected cells were cultured in 6-well plates. Alternatively, the cell population was transfected again using the same method, but pTKhygro (Clontech) and pSVdhfr as resistance plasmids. The expression of GFP was analysed with Fluorescence-activated cell sorter (FACS) and with a Fluoroscan.

Fig.13 shows that the phenotype of the twice-transfected cells (hereafter called secondary transfectants) not only was strongly coloured, such that special bulb and filter were not required to visualize the green color from the GFP protein, but also contained a majority of producing cells (bottom right-hand side FACS histogram) as compared to the parental population (central histogram). This level of fluorescence corresponds to specific cellular productivities of at least 10 pg per cell per day. Indeed,

cells transfected only one time (primary transfectants) that did not express the marker protein were almost totally absent from the cell population after re-transfection. Bars below 10^1 units of GFP fluorescence amounted 30% in the central histogram and less than 5% in the right histogram. This suggested that additional cells had been transfected and successfully expressed GFP.

Strikingly, the amount of fluorescence exhibited by re-transfected cells suggested that the subpopulation of cells having incorporated DNA twice expressed much more GFP than the expected two-fold increase. Indeed, the results shown in Table 2 indicate that the secondary transfectants exhibited, on average, more than the two-fold increase of GFP expected if two sets of sequences, one at each successive transfection, would have been integrated independently and with similar efficiencies. Interestingly, this was not dependent on the promoter sequence driving the reporter gene as both viral and cellular promoter-containing vectors gave a similar GFP enhancement (compare lane 1 and 2). However, the effect was particularly marked for the MAR-containing vector as compared to plasmids without MAR- (lane 3), where the two consecutive transfections resulted in a 5.3 and 4.6 fold increase in expression, in two distinct experiments.

Type of plasmids	Primary transfection	Secondary transfection	EGFP fluorescence Fold increase
pUbCEGFP	4'992	14'334	2.8
pSV40EGFP	4'324	12'237	2.8
pMAR-SV40EGFP	6'996	36'748	**5.3**

Type of plasmids	Primary transfection	Secondary transfection	EGFP fluorescence Fold increase
pUbCEGFP	6'452	15'794	2.5
pSV40EGFP	4'433	11'735	2.6
pMAR-SV40EGFP	8'116	37'475	**4.6**

Table 7. Effect of re-transfecting primary transfectants at 24 hours interval on GFP expression. Two independent experiments are shown. The resistance plasmid pSVneo was co-transfected with various GFP expression vectors. One day post-transfection, cells were re-transfected with the same plasmids with the difference that the resistance plasmid was changed for pSVpuro. Cells carrying both resistance genes were selected on 500 µg/ml G-418 and 5µg/ml puromycin and the expression of the reporter gene marker was quantified by Fluoroscan. The fold increases correspond to the ratio of fluorescence obtained from two consecutive transfections as compared to the sum of fluorescence obtained from the corresponding independent transfections. The fold increases that were judged significantly higher are shown in bold, and correspond to fluorescence values that are consistently over 2-fold higher than the addition of those obtained from the independent transfections.

The increase in the level of GFP expression in multiply tranfected cells was not expected from current knowledge, and this effect had not been observed previously.

Taken together, the data presented here support the idea that the plasmid sequences that primarily integrated into the host genome would facilitate integration of other plasmids by homologous recombination with the second incoming set of plasmid molecules. Plasmid recombination events occur within a 1-h interval after the plasmid DNA has reached the nucleus and the frequency of homologous recombination

between co-injected plasmid molecules in cultured mammalian cells has been shown to be extremely high, approaching unity (Folger, K.R., K. Thomas, and M.R. Capecchi, Nonreciprocal exchanges of information between DNA duplexes coinjected into mammalian cell nuclei. Mol Cell Biol, 1985. 5(1): p. 59-69], explaining the integration of multiple plasmid copies. However, homologous recombination between newly introduced DNA and its chromosomal homolog normally occurs very rarely, at a frequency of 1 in 10^3 cells receiving DNA to the most [Thomas, K.R., K.R. Folger, and M.R. Capecchi, High frequency targeting of genes to specific sites in the mammalian genome. Cell, 1986. 44(3): p. 419-28.]. Thus, the results might indicate that the MAR element surprisingly acts to promote such recombination events. MARs would not only modify the organization of genes in vivo, and possibly also allow DNA replication in conjunction with viral DNA sequences, but they may also act as DNA recombination signals.

Example 14 : MARs mediate the unexpectedly high levels of expression in multiply transfected cells

If MAR-driven recombination events were to occur in the multiple transfections process, we expect that the synergy between the primary and secondary plasmid DNA would be affected by the presence of MAR elements at one or both of the transfection steps. We examined this possibility by multiply transfections of the cells with pMAR alone or in combination with various expression plasmids, using the method described previously. Table 3 shows that transfecting the cells twice with the pMAR-SV40EGFP plasmid gave the highest expression of GFP and the highest degree of enhancement of all conditions (4.3 fold). In contrast, transfecting twice the vector without MAR gave little or no enhancement, 2.8-fold, instead of the expected two-fold increase. We conclude that the presence of MAR elements at each transfection step is necessary to achieve the maximal protein synthesis.

Table 8

Primary transfection		Secondary transfection		
Type of plasmid	EGFP-fluorescence	Type of plasmid	EGFP-fluorescence	Fold increase
pMAR	0	pMAR	0	0
		pSV40EGFP	15'437	**2.3-2.5**
		pMAR-SV40EGFP	30'488	**2.6-2.7**
pMAR-SV40EGFP	11'278	pMAR-SV40EGFP	47'027	**4.3-5.3**
		pMAR	12'319	1.0-1.1
pSV40EGFP	6'114	pSV40EGFP	17'200	2.8
		pMAR	11'169	1.8-2.3

Interestingly, when cells were first transfected with pMAR alone, and then re-transfected with pSV40EGFP or pMAR-SV40EGFP, the GFP levels were more than doubled as compared to those resulting from the single transfection of the later plasmids (2.5 and 2.7 fold respectively, instead of the expected 1-fold). This indicates that the prior transfection of the MAR can increase the expression of the plasmid used in the second transfection procedure. Because MARs act only locally on chromatin structure and gene expression, this implies that the two types of DNA may have integrated at a similar chromosomal locus. In contrast, transfecting the GFP expression vectors alone, followed by the MAR element in the second step, yielded little or no improvement of the GFP levels. This indicates that the order of plasmid

transfection is important, and that the first transfection event should contain a MAR element to allow significantly higher levels of transgene expression.

If MAR elements favoured the homologous recombination of the plasmids remaining in episomal forms from the first and second transfection procedures, followed by their co-integration at one chromosomal locus, one would expect that the order of plasmid transfection would not affect GFP levels. However, the above findings indicate that it is more favourable to transfect the MAR element in the first rather than in the second transfection event. This suggests the following molecular mechanism: during the first transfection procedure, the MAR elements may concatemerize and integrate, at least in part, in the cellular chromosome. This integrated MAR DNA may in turn favour the further integration of more plasmids, during the second transfection procedure, at the same or at a nearby chromosomal locus.

Example 15 : MARs as long term DNA transfer facilitators

If integrated MARs mediated a persistent recombination-permissive chromosomal structure, one would expect high levels of expression even if the second transfection was performed long after the first one, at a time when most of the transiently introduced episomal DNA has been eliminated. To address this possibility, the cells from Table 3, selected for antibiotic resistance for three weeks, were transfected again once or twice and selected for the incorporation of additional DNA resistance markers. The tertiary, or the tertiary and quaternary transfection cycles, were performed with combinations of pMAR or pMAR-SV40EGFP, and analyzed for GFP expression as before.

Table 9

Tertiary transfection			Quaternary transfection		
Type of plasmid	EGFP-fluorescence	Fold increase	Type of plasmid	EGFP-fluorescence	Fold increase
pMAR	18368	**2.2**	pMAR pMAR-SV40EGFP	43'186 140'000	**2.4** **7.6**
pMAR-SV40EGFP	16544	2.0	pMAR-SV40EGFP pMAR	91'000 33'814	**5.5** **2.0**

Table 9. MARs act as facilitator of DNA integration.

The pMAR-SV40EGFP/ pMAR-SV40EGFP secondary transfectants were used in a third cycle of transfection at the end of the selection process. The tertiary transfection was accomplished with pMAR or pMAR-SV40EGFP, and pTKhygro as selection plasmid, to give tertiary transfectants. After 24 hours, cells were transfected again with either plasmid and pSVdhfr, resulting in the quaternary transfectants which were selected in growth medium containing 500 µg/ml G-418 and 5µg/ml puromycin, 300 µg/ml hygromycin B and 5µM methotrexate. The secondary transfectants initially exhibited a GFP fluorescence of 8300. The fold increases correspond to the ratio of fluorescence obtained from two consecutive transfections as compared to the sum of

fluorescence obtained from the corresponding independent transfections. The fold increases that were judged significantly higher are shown in bold, and correspond to fluorescence values that are 2-fold higher than the addition of those obtained from the independent transfections.

These results show that loading more copies of pMAR or pMAR-SV40EGFP resulted in similar 2-fold enhancements of total cell fluorescence. Loading even more of the MAR in the quaternary transfection further enhanced this activity by another 2.4-fold. This is consistent with our hypothesis that newly introduced MAR sequences may integrate at the chromosomal transgene locus by homologous recombination and thereby further increase transgene expression.

When the cells were transfected a third and fourth time with the pMAR-SV40EGFP plasmid, GFP activity further increased, once again to levels not expected from the addition of the fluorescence levels obtained from independent transfections. GFP expression reached levels that resulted in cells visibly glowing green in day light (Fig.14). These results further indicate that the efficiency of the quaternary transfection was much higher than that expected from the efficacy of the third DNA transfer, indicating that proper timing between transfections is crucial to obtain the optimal gene expression increase, one day being preferred over a three weeks period.
We believe that MAR elements favour secondary integration events in increasing recombination frequency at their site of chromosomal integration by relaxing closed chromatin structure, as they mediate a local increase of histone acetylation (Yasui, D., et al., SATB1 targets chromatin remodelling to regulate genes over long distances. *Nature*, 2002. 419(6907): p. 641-5.]. Alternatively, or concomitantly, MARs potentially relocate nearby genes to subnuclear locations thought to be enriched in trans-acting factors, including proteins that can participate in recombination events such as topoisomerases. This can result in a locus in which the MAR sequences can bracket the pSV40EGFP repeats, efficiently shielding the transgenes from chromatin-mediated silencing effects.

Example 16 : Use of MARs identified with SMAR Scan® II to increase the expression of a recombinant protein.

Four MAR elements were randomly selected from the sequences obtained from the analysis of the complete human genome sequence with SMAR Scan® or the combined method. These are termed 1_6, 1_42, 1_68, (where the first number represents the chromosome from which the sequence originates, and the second number is specific to the predicted MAR along this chromosome) and X_S29, a "super" MAR identified on chromosome X. These predicted MARs were inserted into the pGEGFPControl vector upstream of the SV40 promoter and enhancer driving the expression of the green fluorescent protein and these plasmids were transfected into cultured CHO cells, as described previously (Zahn-Zabal, M., et al., *Development of stable cell lines for production or regulated expression using matrix attachment regions.* J Biotechnol, 2001. **87**(1): p. 29-42). Expression of the transgene was then analyzed in the total population of stably transfected cells using a fluorescent cell sorter (FACS) machine. As can be seen from Fig. 19, all of these newly identified MARs increased the expression of the transgene significantly above the expression driven by the chicken lysosyme MAR, the "super" MAR X_S29 being the most potent of all of the newly identified MARs.

Example 17: Effect on hematocrit of *in vivo* expression of mEpo by electrotransfer of Network system with and without Human MAR (1-68).

The therapeutic gene encodes EPO (erythropoietin), an hormone used for the treatment of anemia. The EPO gene is placed under the control of a doxycycline inducible promoter, in a gene switch system described previously called below the Network system (Imhof, M. O., Chatellard, P., and Mermod, N. (2000). A regulatory network for efficient control of transgene expression. J. Gene. Med. **2**, 107-116.). The EPO and regulatory genes are then injected in the muscle of mice using an *in vivo* electroporation procedure termed the electrotransfer, so that the genes are transferred to the nuclei of the muscle fibers. When the doxycycline antibiotic is added to the drinking water of the mice, this compound is expected to induce the expression of EPO, which will lead to the elevation of the hematocrit level, due to the increase in red blood cell counts mediated by the high levels of circulating EPO. Thus, if the MAR improved expression of EPO, higher levels of hematocrit would be expected.

In vivo experiments were carried out on 5 week-old C57BL6 female mice (Iffa Credo-Charles River, France). 30µg of plasmid DNA in normal saline solution was delivered by trans-cutaneous injections in the tibialis anterior muscle. All injections were carried out under Ketaminol (75 mg/kg) and Narcoxyl (10 mg/kg) anesthesia. Following the intramuscular injection of DNA, an electrical field was applied to the muscle. A voltage of 200 V/cm was applied in 8 ms pulses at 1Hz (Bettan M, Darteil R, Caillaud JM, Soubrier F, Delaere P, Branelec D, Mahfoudi A, Duverger N, Scherman D. 2000. "High-level protein secretion into blood circulation after electric pulse-mediated gene transfer into skeletal muscle". *Mol Ther.* **2**: 204-10).

16 mice were injected by the Network system expressing EPO without the 1_68 MAR and 16 other mice were injected with the Network system incorporating the MAR in 5' of the promoter/enhancer sequences driving the expression of the activator and EPO genes. In each group, half of the mice were submitted to doxycycline in drinking water from the beginning of the experiment (day 0 – the day of electrotransfer) and in the other half, doxycycline was put in drinking water starting at day 21.

Blood samples were collected using heparinated capillaries by retro-orbital punction at different times after the injection of plasmids. Capillaries were centrifugated 10 minutes at 5000 rpm at room temperature and the volumetric fraction of blood cells is assessed in comparison to the total blood volume and expressed as a percentile, determining the hematocrit level.

As can be deduced from Fig. 16 The group of mice injected by MAR-network, induced from the beginning of the experiment, display a better induction of the hematocrit in comparison of mice injected by original network without MAR. After 2 months, haematocrits in "MAR-containing group" is still at values higher (65%) than normal hematocrit levels (45-55%).

More importantly, late induction (day 21) is possible only in presence of MAR but not from mice where the Network wwas injected without the MAR. Thus the MAR likely protects the transgenes from silencing and allows induction of its expression even after prolong period in non-inducing conditions.

Overall, the MAR element is able to increase the expression of the therapeutic gene as detected from its increased physiological effect on the hematocrit.

CLAIMS

1. A purified and isolated DNA sequence having protein production increasing activity characterized in that said DNA sequence comprises
a) at least one bent DNA element,
b) and at least one binding site for a DNA binding protein.

2. The purified and isolated DNA sequence of claim 1 characterized in that the bent DNA element contains at least 10% of dinucleotide TA, and/or at least 12% of dinucleotide AT on a stretch of 100 contiguous base pairs.

3. The purified and isolated DNA sequence of claim 2 characterized in that the bent DNA element contains at least 33% of dinucleotide TA, and/or at least 33% of dinucleotide AT on a stretch of 100 contiguous base pairs.

4. The purified and isolated DNA sequence of claims 1 to 2, characterized in that it comprises a MAR nucleotide sequence selected from the group comprising the sequences SEQ ID Nos 1 to 27, a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.

5. The purified and isolated DNA sequence of claims 1 to 2, characterized in that it comprises a cLysMAR element and/or fragment, a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.

6. The purified and isolated DNA sequence of claim 5, characterized in that said part thereof is a nucleotide sequence selected from the B, K and F regions.

7. The purified and isolated sequence of claims 1 to 6, characterized in that said DNA binding protein is a transcription factor.

8. The purified and isolated sequence of claim 7, characterized in that the transcription factor is selected from the group comprising the polyQpolyP domain proteins.

9. The purified and isolated sequence of claim 7, characterized in that the transcription factor is selected from the group comprising SATB1, NMP4, MEF2, S8, DLX1, FREAC7, BRN2, GATA 1/3, TATA, Bright, MSX, AP1, C/EBP, CREBP1, FOX, Freac7, HFH1, HNF3alpha, Nkx25, POU3F2, Pit1, TTF1, XFD1, AR, C/EBPgamma, Cdc5, FOXD3, HFH3, HNF3 beta, MRF2, Oct1, POU6F1, SRF, V$MTATA_B, XFD2, Bach2, CDP CR3, Cdx2, FOXJ2, HFL, HP1, Myc, PBX, Pax3, TEF, VBP, XFD3, Brn2, COMP1, Evil, FOXP3, GATA4, HFN1, Lhx3, NKX3A, POU1F1, Pax6, TFIIA and Vmw65 or a combination of two or more of these transcription factors.

10. A purified and isolated cLysMAR element and/or fragment having protein production increasing activity, a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.

11. The cLysMAR element and/or fragment of claim 10 consisting of at least one nucleotide sequence selected from the B, K and F regions.

12. A synthetic MAR sequence comprising natural MAR elements and/or fragments assembled between linker sequences.

13. The synthetic MAR sequence of claim 12, characterized in that the MAR comprises a cLysMAR element and/or fragment, a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.

14. The synthetic MAR sequence of claims 12 to 13, characterized in that the linker sequences are BglII-BamHI linker.

15. A method for identifying a MAR sequence using a Bioinformatic tool comprising the computing of values of one or more DNA sequence features corresponding to DNA bending, major groove depth and minor groove width potentials and melting temperature.

16. The method for identifying a MAR sequence using a Bioinformatic tool according to claim 15, characterized in that said Bioinformatic tool contains algorithms, adapted to the use of profiles or weight-matrices, to compute values for one or more of said DNA sequence features corresponding to DNA bending, major groove depth and minor groove width potentials, and melting temperature.

17. The method for identifying a MAR sequence using a Bioinformatic tool according to claim 16, characterized in that said profiles or weight-matrices are based on dinucleotide recognition.

18. The method for identifying a MAR sequence using a Bioinformatic tool according to claim 17, characterized in that said Bioinformatic tool computes values for all of said DNA sequence features,

19. The method for identifying a MAR sequence using a Bioinformatic tool according to claim 18, characterized in that said Bioinformatic tool is SMAR Scan®®.

20. The method for identifying a MAR sequence using a Bioinformatic tool according to claims 15-19, characterized in that the identification of one or more DNA sequence features further comprises a feature corresponding to one or more binding sites for DNA binding proteins.

21. The method for identifying a MAR sequence using a Bioinformatic tool according to claim 20, characterized in that said DNA binding protein is a transcription factor.

22. The method for identifying a MAR sequence using a Bioinformatic tool according to claim 21, characterized in that the transcription factor is selected from the group comprising polyQpolyP domain proteins or transcription factors.

23. The method for identifying a MAR sequence using a Bioinformatic tool according to claims 20 to 21, characterized in that the DNA binding protein is selected from the group comprising SATB1, NMP4, MEF2, S8, DLX1, FREAC7, BRN2, GATA 1/3, TATA, Bright, MSX, AP1, C/EBP, CREBP1, FOX, Freac7, HFH1, HNF3alpha, Nkx25, POU3F2, Pit1, TTF1, XFD1, AR, C/EBPgamma, Cdc5, FOXD3, HFH3, HNF3 beta, MRF2, Oct1, POU6F1, SRF, V$MTATA_B, XFD2, Bach2, CDP CR3, Cdx2, FOXJ2, HFL, HP1, Myc, PBX, Pax3, TEF, VBP, XFD3, Brn2, COMP1, Evil, FOXP3, GATA4,

HFN1, Lhx3, NKX3A, POU1F1, Pax6, TFIIA and Vmw65 or a combination of two or more of these transcription factors.

24. The method for identifying a MAR sequence using a Bioinformatic tool according to claims 15-23, characterized in that values for the identification of DNA bending are comprised between 3 to 5 °.

25. The method for identifying a MAR sequence using a Bioinformatic tool according to claim 24, characterized in that values for the identification of DNA bending are comprised between 3.8 to 4.4 °.

26. The method for identifying a MAR sequence using a Bioinformatic tool according to claims 15-25 characterized in that values for the identification of the major groove depth are comprised between 8.9 to 9.3 Å and values for the identification of minor groove width are comprised between 5.2 to 5.8 Å.

27. The method for identifying a MAR sequence using a Bioinformatic tool according to claims 26, characterized in that values for the identification of major groove depth are comprised between 9.0 to 9.3 Å and values for the identification of minor groove width are comprised between 5.4 to 5.7 Å.

28. The method for identifying a MAR sequence using a Bioinformatic tool according to claims 15-27, characterized in that the melting temperature is comprised between 55 to 75 ° C.

29. The method for identifying a MAR sequence using a Bioinformatic tool according to claim 28, characterized in that the melting temperature is comprised between 55 to 62 ° C.

30. The method for identifying a MAR sequence using a Bioinformatic tool of claims 15 to 29, characterized in that it further comprises at least one filter predicting DNA binding sites for DNA transcription factors.

31. The method for identifying a MAR sequence using a Bioinformatic tool according to claim 30, characterized in that the filter is applied before or after the Bioinformatic tool.

32. The method according to claims 30 to 31, characterized in that the filter detects clusters of DNA binding sites using profiles or weightmatrices.

33. The method according to claim 32, characterized in that the filter detects densities of clusters of DNA binding sites.

34. A method for identifying a MAR sequence characterized in that it comprises at least one filter detecting clusters of DNA binding sites using profiles or weightmatrices.

35. A purified and isolated MAR DNA sequence identifiable according to claims 15 to 33 or claim 34.

36. The purified and isolated MAR DNA sequence of claim 35, containing at least 10% of dinucleotide TA on a stretch of 100 contiguous base pairs.

37. The purified and isolated MAR DNA sequence of claim 36, containing at least 33% of dinucleotide TA on a stretch of 100 contiguous base pairs.

38. The purified and isolated MAR DNA sequence of claims 35 to 37, further containing at least 12% of dinucleotide AT on a stretch of 100 contiguous base pairs.

39. The purified and isolated MAR DNA sequence of claim 38, further containing at least 33% of dinucleotide AT on a stretch of 100 contiguous base pairs.

40. The purified and isolated MAR DNA sequence of any of claims 35 to 39, comprising a sequence selected from the sequences SEQ ID Nos 1 to 27, a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.

41. The purified and isolated DNA sequence of claim 40, comprising a sequence selected from the sequences SEQ ID Nos 24 to 27, a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.

42. The use of a purified and isolated DNA sequence comprising a first isolated matrix attachment region (MAR) nucleotide sequence which is a MAR nucleotide sequence selected from the group comprising:

- a purified and isolated DNA sequence of claims 1 to 9,
- a purified and isolated MAR DNA of claims 35 to 41,
- the sequences SEQ ID Nos 1 to 27,
- a purified and isolated cLysMAR element and/or fragment,
- a synthetic MAR sequence of claims 12 to 14,

a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants for increasing protein production activity in a eukaryotic host cell.

43. The use of the purified and isolated DNA sequence of claim 42, characterized in that said purified and isolated DNA sequence further comprises a promoter operably linked to a gene of interest.

44. The use of the purified and isolated DNA sequence of claims 42 or 43, characterized in that said purified and isolated DNA sequence further comprises at least a second isolated matrix attachment region (MAR) nucleotide sequence which is a MAR nucleotide sequence selected from the group comprising:

- a purified and isolated DNA sequence of claims 1 to 9,
- a purified and isolated MAR DNA of claims 35 to 41,
- the sequences SEQ ID Nos 1 to 27,
- a purified and isolated cLysMAR element and/or fragment,
- a synthetic MAR sequence of claims 12 to 14,

a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants for increasing protein production activity in a eukaryotic host cell.

45. The use of the purified and isolated DNA sequence of claim 44, characterized in that said first and at least second MAR sequences are located at both the 5' and the 3' ends of the sequence containing the promoter and the gene of interest.

46. The use of the purified and isolated DNA sequence of claim 44, characterized in that said first and or at least second MAR sequences are located on a sequence distinct from the one containing the promoter and the gene of interest.

47. The use of the purified and isolated DNA sequence of any of claims 42 to 46, characterized in that said purified and isolated DNA sequence is in the form of a linear DNA sequence as vector.

48. A method for transfecting a eukaryotic host cell, said method comprising
a) introducing into said eukaryotic host cell at least one purified DNA sequence comprising at least one DNA sequence of interest and/or at least one purified and isolated DNA sequence consisting of a MAR nucleotide sequence or other chromatin modifying elements,
b) subjecting within a defined time said transfected eukaryotic host cell to at least one additional transfection step with at least one purified DNA sequence comprising at least one DNA sequence of interest and/or with at least one purified and isolated DNA sequence consisting of a MAR nucleotide sequence or other chromatin modifying elements
c) selecting said transfected eukaryotic host cell.

49. The method of claim 48, characterized in that said DNA sequence of interest is a gene of interest coding for a protein operably linked to a promoter.

50. The method of claims 48 and 49, characterized in that the selected transfected eukaryotic host cells are high protein producer cells with a production rate of at least 10 pg per cell per day.

51. The method of claims 48-50, characterized in that the MAR nucleotide sequence is selected from the group comprising:
- a purified and isolated DNA sequence of claims 1 to 9,
- a purified and isolated MAR DNA of claims 35 to 41,
- the sequences SEQ ID Nos 1 to 27,
- a purified and isolated cLysMAR element and/or fragment,
- a synthetic MAR sequence of claims 12 to 14,

a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.

52. The method of claims 48-50, characterized in that the MAR nucleotide is a purified and isolated sequence according to claims 1 to 9, a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.

53. The method of claims 48 to 52, characterized in that the defined time corresponds to intervals related to the cell division cycle.

54. The method of claim 53, characterized in that the defined time is the moment the host cell just has entered into a second cell division cycle.

55. A method for transfecting a eukaryotic host cell, said method comprising co-transfecting into said eukaryotic host cell at least one first purified and isolated DNA sequence comprising at least one DNA sequence of interest, and a second and isolated purified DNA comprising at least one MAR nucleotide selected from the group comprising:

- a purified and isolated DNA sequence of claims 1 to 9,
- a purified and isolated MAR DNA of claims 35 to 41,
- the sequences SEQ ID Nos 1 to 27,
- a purified and isolated cLysMAR element and/or fragment,
- a synthetic MAR sequence of claims 12 to 14,

a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.

56. A process for the production of a protein wherein
a) a eukaryotic host cell transfected according to claims 48 to 54 or claim 55, is cultured in a culture medium under conditions suitable for expression of said protein and
b) said protein is recovered.

57. A eukaryotic host cell transfected according to any one of claims 48 to 54 or claim 55.

58. A cell transfection mixture or kit comprising at least one purified and isolated DNA sequence according to claims 1 to 9, 10 to 11, 12 to 14 or 35 to 41.

59. A transgenic organism characterized in that at least some of its cells have stably incorporated at least one DNA sequence of claims 1 to 9, 10 to 11, 12 to 14 or 35 to 41.

60. A transgenic organism characterized in that its genome has stably incorporated at least one DNA sequence of claims 1 to 9, 10 to 11, 12 to 14 or 35 to 41.

61. The transgenic organism of claims 59 and 60 characterized in that some of its cells have been transfected according to the method of claims 48 to 54 or claim 55.

62. A computer readable medium characterized in that it comprises computer-executable instructions for performing the method for identifying a MAR sequence of claims 15 to 33 and/or claim 34.

FIG.1

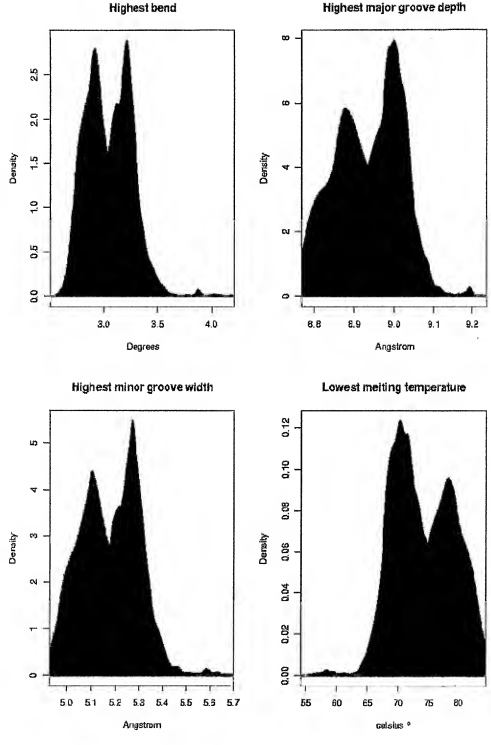

Highest bend
Density
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
Degrees
Highest major groove depth
Density
0
2
4
6
8
8.8
8.9
9.0
9.1
9.2
Angstrom
Highest minor groove width
Density
0
1
2
3
4
5
5.0
5.1
5.2
5.3
5.4
5.5
5.6
5.7
Angstrom
Lowest melting temperature
Density
0.00
0.02
0.04
0.06
0.08
0.10
0.12
55
60
65
70
75
80
celsius °

FIG.2

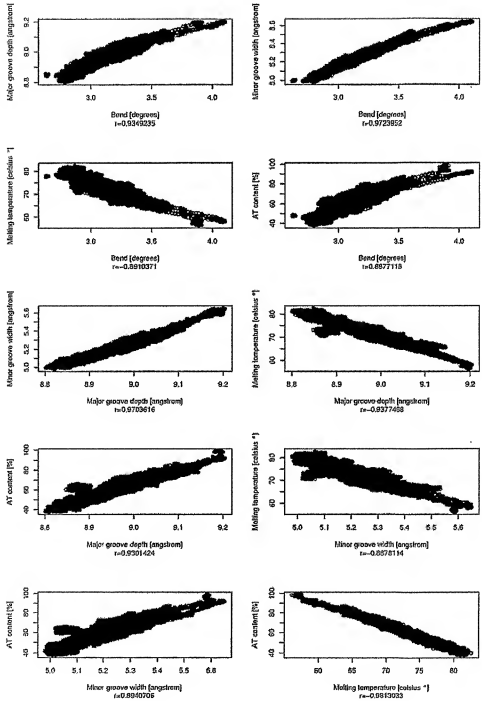

Major groove depth [angstrom]
Bend [degrees]
r=0.9349335
Minor groove width [angstrom]
Bend [degrees]
r=0.9723952
Melting temperature [celsius °]
Bend [degrees]
r=-0.8910371
AT content [%]
Bend [degrees]
r=0.8577118
Minor groove width [angstrom]
Major groove depth [angstrom]
r=0.9709616
Melting temperature [celsius °]
Major groove depth [angstrom]
r=-0.8377468
AT content [%]
Major groove depth [angstrom]
r=0.9391424
Melting temperature [celsius °]
Minor groove width [angstrom]
r=-0.8578114
AT content [%]
Minor groove width [angstrom]
r=0.8940706
AT content [%]
Melting temperature [celsius °]
r=-0.8913033

FIG.3

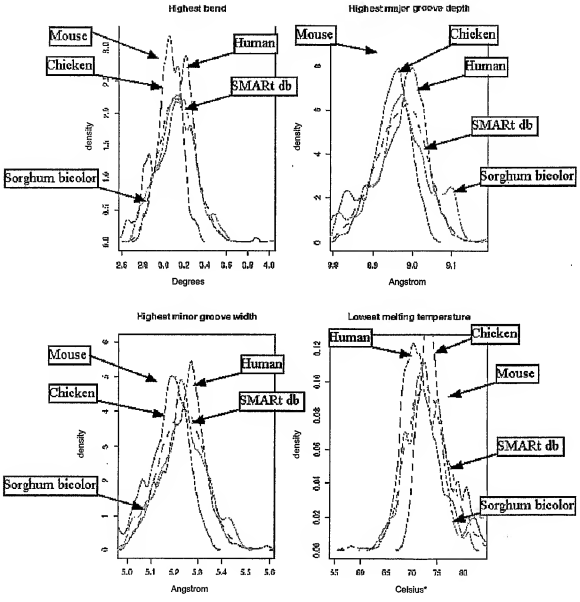

Highest bend
Mouse
Chicken
Human
SMARt db
Sorghum bicolor
density
Degrees
Highest major groove depth
Mouse
Chicken
Human
SMARt db
Sorghum bicolor
density
Angstrom
Highest minor groove width
Mouse
Chicken
Human
SMARt db
Sorghum bicolor
density
Angstrom
Lowest melting temperature
Human
Chicken
Mouse
SMARt db
Sorghum bicolor
density
Celsius°

FIG.4

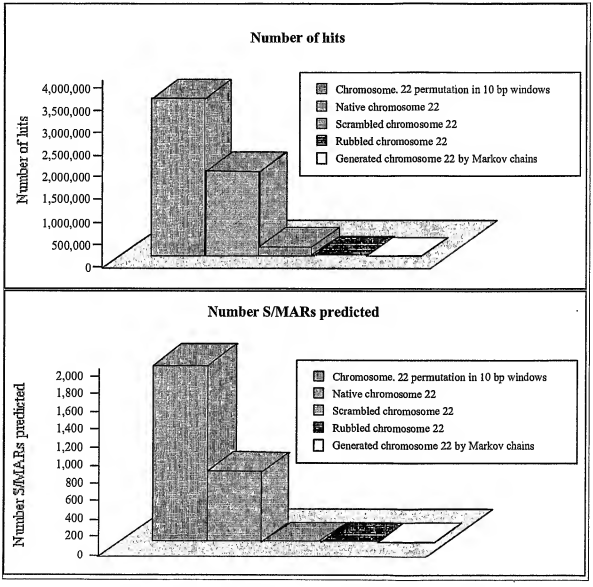

Number of hits
Number of hits
4,000,000
3,500,000
3,000,000
2,500,000
2,000,000
1,500,000
1,000,000
500,000
0
Chromosome. 22 permutation in 10 bp windows
Native chromosome 22
Scrambled chromosome 22
Rubbled chromosome 22
Generated chromosome 22 by Markov chains
Number S/MARs predicted
Number S/MARs predicted
2,000
1,800
1,600
1,400
1,200
1,000
800
600
400
200
0
Chromosome. 22 permutation in 10 bp windows
Native chromosome 22
Scrambled chromosome 22
Rubbled chromosome 22
Generated chromosome 22 by Markov chains

FIG.5

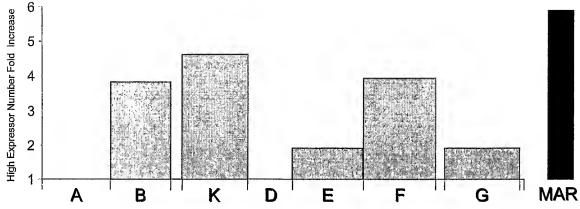

High Expressor Number Fold Increase
6
5
4
3
2
1
A
B
K
D
E
F
G
MAR

FIG.6

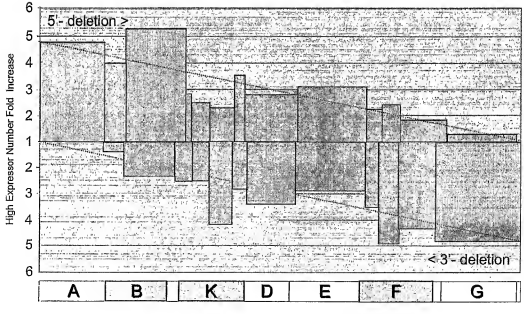

High Expressor Number Fold Increase
6
5
4
3
2
1
2
3
4
5
6
5' - deletion >
< 3' - deletion
A
B
K
D
E
F
G

FIG.7

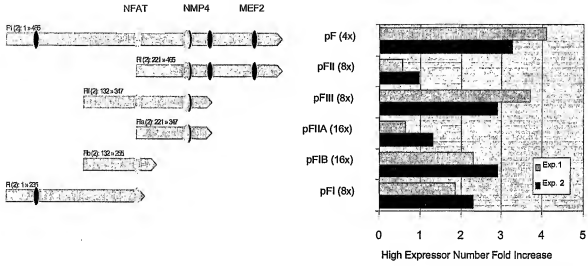

NFAT
NMP4
MEF2
Fl(2) 1×455
Fl(2) 221×455
Fl(2) 132×397
Fl(2) 221×397
Fl(2) 132×226
Fl(2) 1×226
pF (4x)
pFII (8x)
pFIII (8x)
pFIIA (16x)
pFIB (16x)
pFI (8x)
Exp. 1
Exp. 2
0
1
2
3
4
5
High Expressor Number Fold Increase

FIG.8

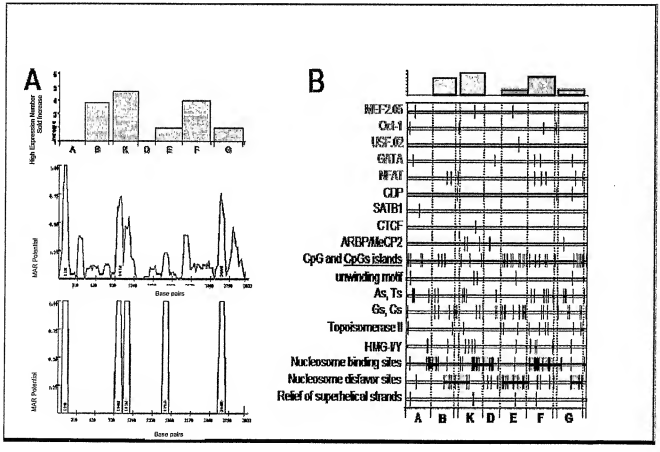
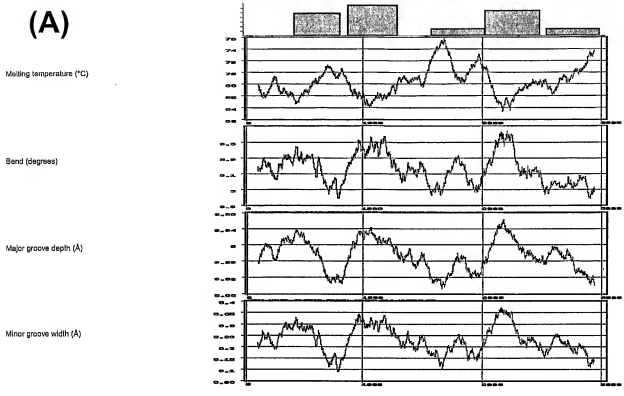

A
High Expression Number Fold Increase
A
B
K
D
E
F
G
MAR Potential
Base pairs
B
MEF2-05
Oct-1
USF-02
GATA
NFAT
CDP
SATB1
CTCF
ARBP/MeCP2
CpG and CpGs islands
unwinding motif
As, Ts
Gs, Cs
Topoisomerase II
HMG-I/Y
Nucleosome binding sites
Nucleosome disfavor sites
Relief of superhelical strands
A
B
K
D
E
F
G

FIG.9

(A)


Melting temperature (°C)
Bend (degrees)
Major groove depth (Å)
Minor groove width (Å)

(B)

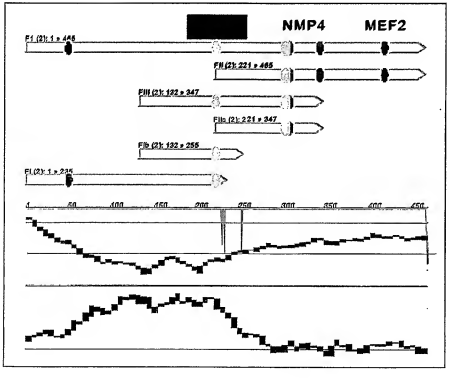

NMP4
MEF2
F1 (2): 1 » 446
FII (2): 221 » 465
FIII (2): 122 » 347
FIb (2): 221 » 347
Fb (2): 122 » 255
FI (2): 1 » 235

FIG.10

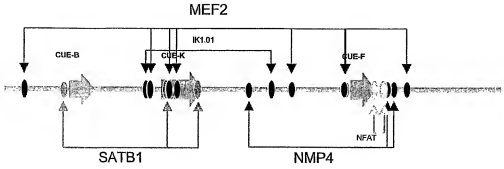

MEF2
IK1.01
CUE-B
CUE-K
CUE-F
NFAT
SATB1
NMP4

FIG.11

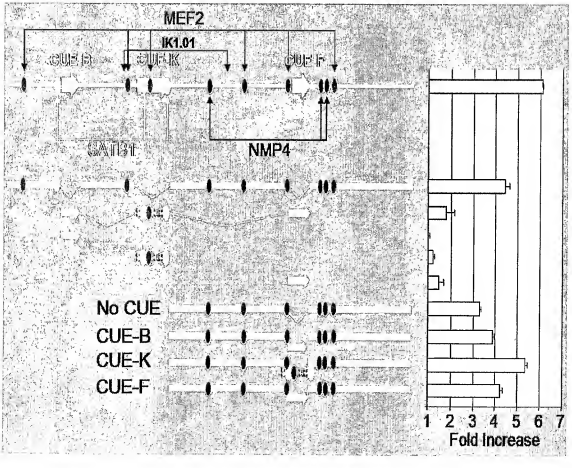

MEF2
IK1.01
CUE-B
CUE-K
CUE-F
SATB1
NMP4
No CUE
CUE-B
CUE-K
CUE-F
1 2 3 4 5 6 7
Fold Increase

FIG.12

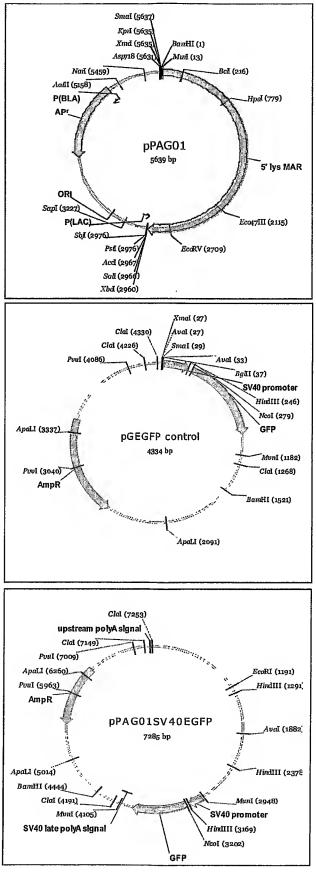

pPAG01
5639 bp
SmaI (5637)
KpnI (5633)
XmaI (5632)
Asp718 (5631)
BamHI (1)
MunI (13)
BclI (216)
HpaI (779)
5' lys MAR
EcoT38I (2115)
EcoRV (2709)
PstI (2975)
AccI (2967)
SalI (2966)
XbaI (2960)
SacI (2957)
SbfI (2976)
OR(
P(LAC)
AP(
P(BLA)
AatII (5558)
NsiI (5459)
pGEGFP control
4334 bp
XmaI (27)
AvaI (27)
SmaI (29)
AvaI (33)
BglII (37)
SV40 promoter
HindIII (246)
NcoI (279)
GFP
MunI (1182)
ClaI (1268)
BamHI (1531)
ApaLI (2091)
ClaI (4330)
ClaI (4226)
PvuI (4086)
ApaLI (3337)
PvuI (3040)
AmpR
pPAG01SV40EGFP
7286 bp
ClaI (7253)
upstream polyA signal
ClaI (7149)
PvuI (7009)
ApaLI (6269)
PvuI (5963)
AmpR
EcoRI (1191)
HindIII (1291)
AvaI (1888)
HindIII (2376)
MunI (3048)
SV40 promoter
HindIII (3169)
NcoI (3202)
GFP
ApaLI (5014)
BamHI (4444)
ClaI (4191)
MunI (4105)
SV40 late polyA signal

FIG.13

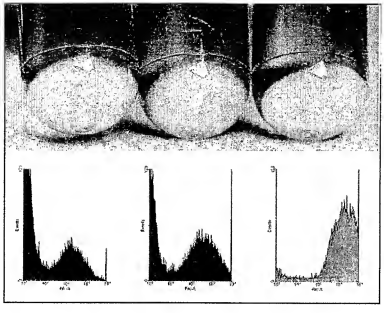


FIG.14

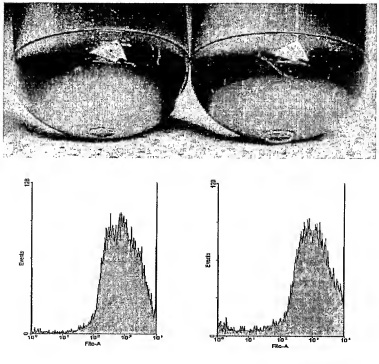


FIG.15

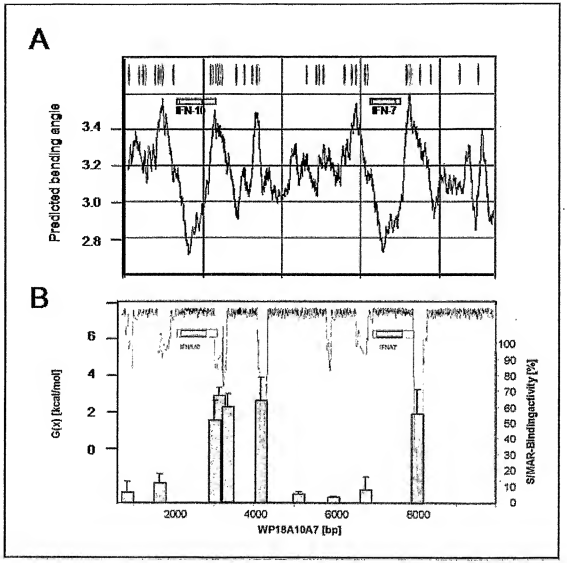

A
Predicted bending angle
3.4
3.2
3.0
2.8
IFN-10
IFN-7
B
G(x) [kcal/mol]
6
4
2
0
SMAR
IFNA7
100
90
80
70
60
50
40
30
20
10
0
SMAR-Bindingactivity [%]
2000
4000
6000
8000
WP18A10A7 [bp]

FIG.16

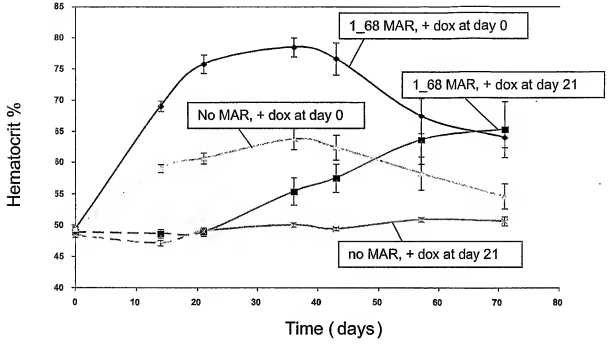
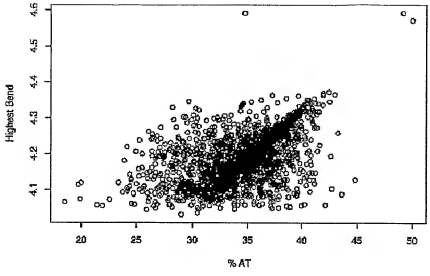

Hematocrit %
Time (days)
1_68 MAR, + dox at day 0
1_68 MAR, + dox at day 21
No MAR, + dox at day 0
no MAR, + dox at day 21
85
80
75
70
65
60
55
50
45
40
0
10
20
30
40
50
60
70
80

FIG.17


Highest Bend
4.1
4.2
4.3
4.4
4.5
4.6
20
25
30
35
40
45
50
% AT

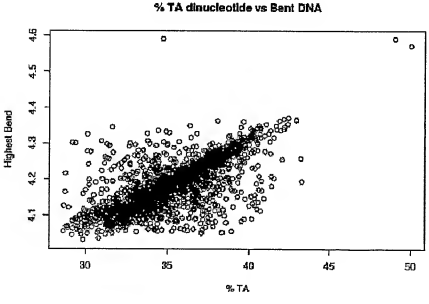
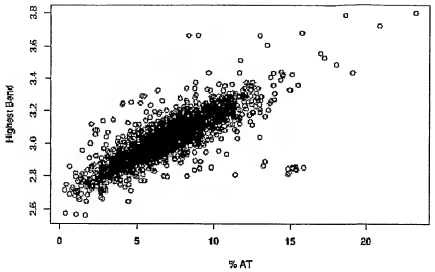

% TA dinucleotide vs Bent DNA
Highest Bend
4.1
4.2
4.3
4.4
4.5
4.6
30
35
40
45
50
% TA

FIG.18


Highest Bend
2.6
2.8
3.0
3.2
3.4
3.6
3.8
0
5
10
15
20
% AT

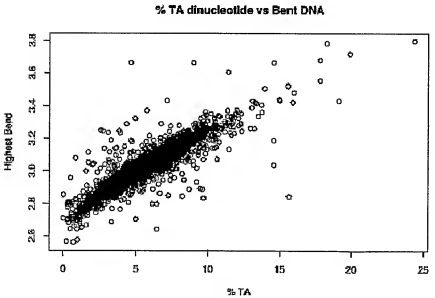

% TA dinucleotide vs Bent DNA
Highest Bend
2.6
2.8
3.0
3.2
3.4
3.6
3.8
0
5
10
15
20
25
% TA

FIG.19

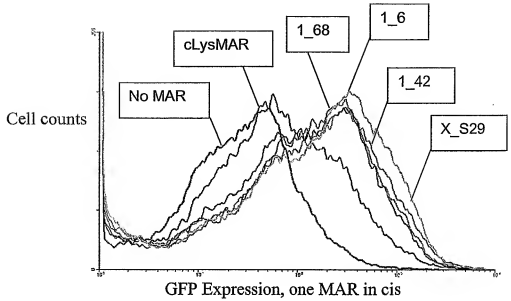
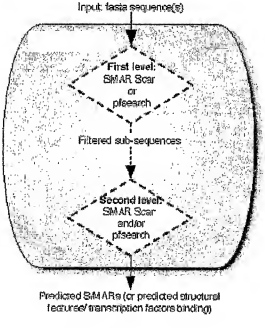

cLysMAR
1_68
1_6
No MAR
1_42
X_S29
Cell counts
GFP Expression, one MAR in cis

FIG.20


Input: fasta sequence(s)
First level: SMAR Scar or pfsearch
Filtered sub-sequences
Second level: SMAR Scar and/or pfsearch
Predicted SMARs (or predicted structural features/ transcription factors binding)

SEL PCT 012.ST25
SEQUENCE LISTING

<110> Selexis S.A.

<120> HIGH EFFICIENCY GENE TRANSFER AND EXPRESSION IN MAMMALIAN CELLS BY A MULTIPLE TRANSFECTION PROCEDURE OF MAR SEQUENCES

<130> SEL PCT 012

<150> US 60/513,574

<151> 2003-10-24

<150> EP 04 002 722.9

<151> 2004-02-06

<160> 241

<170> PatentIn version 3.1

<210> 1

<211> 320

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

SEL PCT 012.ST25

<222> (1)..(320)

<223> MAR of human chromosome 1, nt from 36686 to 37008

<220>

<221> misc_binding

<222> (1)..(320)

<223> MAR of human chromosome 1, genomic contig; 36686 to 37008

<400> 1
ttatattatg ttgttatata tattatatta tgttattaga ttatattatg ttgttatatt 60

atataataat attatattat atattatata ttatattata taatatataa taatattata 120

taattatata ttacattata taatatataa taatattata taattatata ttacattata 180

taatatataa taatattata taataatata taattatata atatataata atattatata 240

atattatata atattatata atatataaat atataataat atatattata ttatataata 300

gtatataata ttatataata 320

<210> 2

<211> 709

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(709)

<223> MAR of human chromosome 1, nt from 142276 to 142984

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(709)

<223> MAR of human chromosome 1, genomic contig; 142276 to 142984

<400> 2
tacaatatat tttctattat atatattttg tattatatat aatatacaat atattttcta 60

ttatatataa tatattttgt attatatata ttacaatata ttttgtatta tataatatat 120

aatacaatat ataatatatt gtattatata ttatataata caatatatta tatattgtat 180

tatatattat atataatact atataatata ttgtattata tattatatat aatactatat 240

aatatatttt attatatatt atatataata caatatataa tatattgtat tataatacaa 300

tgtattataa tgtattatat tgtattatat attatatata atacaatata taataatata 360

ttataatata taataataat ataatataat aataatatat attgtattat atattatata 420

atacaatata taatatattg tattatatat attttattac atataatata taatacatta 480

tataatatat tttgtattat atataatata ttttattatg tattatagat aatatatttt 540

attatatatt atatataata caatatataa tatattttgt attgtatata atatataata 600

caatatataa tatattgtat tatatataat attaatatat tttgtattat atatttatat 660

tttatattat aattatgttt tgcattatat atttcatatt atatatacc 709

<210> 3

<211> 409

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

SEL PCT 012.ST25

<222> (1)..(409)

<223> MAR of human chromosome 1, nt from 1368659 to 1369067

<220>

<221> misc_binding

<222> (1)..(409)

<223> MAR of human chromosome 1, genomic contig; 1368659 to 1369067

<400> 3
tacacataaa tacatatgca tatatattat gtatatatac ataaatacat atgcatatac 60

attatgtata tatacataaa tacatatgca tatacattat gtatatatac ataaatacat 120

atgcatatac attatgtata tatacataaa tacatatgca tatacattat gtatatatac 180

ataaatacat atgcatatac attatgtata tatacataaa tacatatgca tatacattat 240

gtatatatac ataaatacat atgcatatat tatatacata aattatatta tatacataat 300

acatatacat atattatgtg tatatataca taaatacata tacatatatt atgtgtatat 360

atacatgata catatacata tattatgtat atatatacat aaatacata 409

<210> 4

<211> 394

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(394)

<223> MAR of human chromosome 1, genomic contig; 2839089 to 2839482

<400> 4
tatgtatata tacacacata tgtatatata cacacatatg tatatacgta tatatgtata 60

tatacacaca tatgtatata cgtatatatg tatatataca cacatatgta tatacgtata 120

tatgtatata tacacacata tgtatatacg tatatatgta tatatacaca catatgtata 180

tatgtatata tacacacata tgtatatacg tatatatgta tatatacaca catgtgtata 240

tatatataca catatgtata tatgtatata tacacacata tgtatatatg tgtatgtata 300

tatacacaca tatgtatata tacacatata tatgtatata tacacacata cttatatata 360

cacatatata tgtatatata cacatatgta taca 394

<210> 5

<211> 832

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(832)

<223> MAR of human chromosome 1, genomic contig; 1452269 to 1453100

<400> 5
tatattacta tatatacaat atacatatta ctatatatac catgtattac tatatatatc 60

tactatatat attactatat atacaaaata tatattacta tatatacaat atacatatta 120

ctatatatac catatattac tatatatatc tactatatat attactatat atacaaaata 180

tatattacta tatatactat atattactgt atatacaata tatattacta tatatatact 240

atatattact atatatacac tatatattac tatatataca caatatatat attactatat 300

SEL PCT 012.ST25

atacacaatg tatataacta tatatacaat atatattact atatatacta tatatattac 360

tatacatact atatattact ctatatatac aatatatata ttacaatata tactacatat 420

tactacatat actttatata ttactatata tactatatat tactgtatat acaatatata 480

ttactaaata tacacaatat atattactat atatacacaa tatatatatt actatatata 540

cacattatat atgactatat atacacacta tatatattac tatatataca caatatataa 600

ctatatatac acagtataca tattactata tatacacaat atatatatta ctatatatac 660

actatatatt actatatata cacaatatat attactctat gtatacacta tatatattac 720

tatatataca gaatatatat aactatatat acactatatt actatatata ctatatatta 780

ctatatgtac tatatatatt actatatata ctatatatta ctatatatac ac 832

<210> 6

<211> 350

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(350)

<223> MAR of human chromosome 1, genomic contig; 831495 to 831844

<400> 6

aatatataat atataaatat taatatgtat tatataatat atattaatat attatattat 60

attactatat aaataatatt aatatattat attaaaatat taataaatat atcatattaa 120

atattatatt aattaaatat taataaatat attatattaa tatatttata tattaaacct 180

ataacatatg catatactta tttatatata acatgcatgt acttatttat atatacaata 240

tatatttata tattatataa tatattatat gtatttatat attatatatc atatattata 300

tgtatttata tattatatat catataatat atatatttat attatatata 350

<210> 7

<211> 386

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(386)

<223> MAR of human chromosome 1, genomic contig; 1447225 to 1447610

<400> 7
acatttaatt taattatata ctgctatata taattaaatc tatatatcta tataacttat 60

aatttatttt aatttaatta tatatactat atagttatat atacatatat gtaattatat 120

atagtataat tatagtatat atgtatatat aatgtaagta aatatatagt atatatttat 180

atatactata tatttataca tatgtcttta tatatactaa tatatataca catatgtaat 240

atgtacatat ggcatatatt ttatagtgta tatatacata tatgtaatat atatagtaat 300

atgtaaatat atagtacata tttaattata tggtaatata tacacatata tgtaatatgt 360

gtattatagt acatatttta tagtat 386

<210> 8

<211> 585

<212> DNA

<213> Homo sapiens

<220>

SEL PCT 012.ST25

<221> misc_binding

<222> (1)..(585)

<223> MAR of human chromosome 1, genomic contig; 4955365 to 4955949

<400> 8
atacacacat atacacatat gtacgtatat atactatata tacacacata tacacatatg 60

tacgtatata tactatatat acacacatat acacatatgt acgtatatat actatatata 120

cacacatata cacatatgta cgtatatata ctatatatac acacatatac acatatgtac 180

gtatatatac tatatataca cacatataca catatgtacg tatatattat atatacacac 240

atatacacat atgtacgtat atatactata tatacacaca tatacacata tgtacgtata 300

tatactatat atacacacat atacacatat gtacgtatat atactatata tacacacata 360

tacacatatg tacgtatata tactatatat acacacatat acacatatgt acgtatatat 420

actatatata cacacatata cacatatgta cgtatatata ctatatatac acacatatac 480

acatatgtac gtatatatac tatatataca cacatataca catatgtacg tatatatact 540

atatataccc atacacatac gtatatacgt acatatatat acgta 585

<210> 9

<211> 772

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(772)

<223> MAR of human chromosome 1, genomic contig; 5971862 to 5972633

SEL PCT 012.ST25

<400> 9
agtaaacata tatatagtaa atatatatag tgtatatata gtaaatatat atagtgcata 60

tatatagtgc atatatatag tgtatatata gtaaatatat agtgtatata tatagtaaat 120

atatatagtg tatatatagt aaatatatat agtaaatata tatatactat atatagtaaa 180

tatatatata ctatatatag taaatatata tatagtatat atatagtaaa tatatatata 240

gtatatatat agtaaatata tatatagtat atatatagta aatatatata tagtatatat 300

agtaaatata tatagtatat atatagtaaa tatatatata gtatatatat agtaaatata 360

tatatagtat atatatagta aatatatata tagtatatat atagtaaata tatatagtat 420

atatatagta aatatatata gtatatatat agtaaatata tatagtatat atatagtaaa 480

tatatataca ctgtatatat atagtaaata tatatacact gtatatatat agtaaatata 540

tatacactgt atatatatag taaatatata tacactgtat atatatagta aatatatata 600

cactgtatat acatagtaaa tatatataca ctgtatatac atagtaaata tatatacact 660

gtatatacat agtaaatata tatacactgt atatacatag taaatatata tacagtgtat 720

atacatagta aatatatata cagtgtatat acatagtaaa tatatataca gt 772

<210> 10

<211> 304

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(304)

<223> MAR of human chromosome 1, genomic contig; 6221897 to 6222200

<400> 10

SEL PCT 012.ST25

atatataata tatataatta tattatatat aatatataat atatataatt atattatata 60

ttatatataa tatattatat attatatata taatatatat tatatattaa atatatatta 120

tatatataat atatattata tattaaatat atattatata tataatatat attatatata 180

atatatataa tatatattat atatatatta tatattatat atatatatta tatatatata 240

atatatataa tatatattat atataatata tattatatat atataatata tataatatat 300

atta 304

<210> 11

<211> 311

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(311)

<223> MAR of human chromosome 1, genomic contig; 9418531 to 9418841

<400> 11

tatatataat atttatatat aatattcatg tatttatata taaatattta tatatttata 60

tataaatatt tatatattta tatataaata tttatatatt tatatataat atttatacat 120

tatatataat atttatatat tatatataat atttatatat aatatttata tattatatat 180

aatatttata tatttatatg tataatatat attttatata tgtatgtata atatatattt 240

tatatatgta tgtataatat attttatata tgtatgtata atatattatt atatataata 300

tataatttat a 311

<210> 12

<211> 302

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(302)

<223> MAR of human chromosome 1, genomic contig; 15088789 to 15089090

<400> 12
atataatata tatattatat atataaatat atataaatat ataacatata tattatatat 60

aaatatatat aaatatataa catatatatt atatatataa atatatataa atatataaca 120

tatatattat atatataaat atatataaat atataacata tatattatat atataaatat 180

atattatata tttatatata taatatatat aaatatataa tatatattta tatatataat 240

atatataaat atataatata tatatttata tataatatat ataaatatat aatatataat 300

at 302

<210> 13

<211> 461

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(461)

<223> MAR of human chromosome 1, genomic contig; 6791827 to 6792287

SEL PCT 012.ST25

<400> 13
tatataatat atattatata tacacatata taatatatat tatatataca catatataat 60

atatattata tatacacata tataatatat attatatata cacatatata atatatatta 120

tatatacaca tatataatat atattatata tacacatata taatatatat tatatataca 180

catatataat atatattata tatacacata tataatatat attatatata cacatatata 240

atatatatta tatatacaca tatgtaatat atattataca cacacatata atatatatta 300

tatacacata tataatatat attatatata catatataat atatattata tatacacata 360

tataatatat attatatata cacatatata atatatatta tatatacaca tataatatat 420

aatatataca catatataat atatatatta tatatgcaca t 461

<210> 14

<211> 572

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(572)

<223> MAR of human chromosome 1, genomic contig; 163530 to 164101

<400> 14
atattataat tatatatatt atatataatt atataaaata tatattataa ttatatatat 60

tttatataat atatatatta taattaatat attatatata atatatatat tatatataat 120

atatatatta tatatattat atataatata tataatatat ataatatata atataatata 180

tatattatat ataatatata atatatataa tatattataa tataatatat ataatatata 240

atataatata tataatatat aatataatat ataatatata atatatataa tatataatat 300

SEL PCT 012.ST25

aatatataat atatataata tataatataa tatataatat atataatata ttataatata 360

atatatataa tatataatat aatatatata atatataata taatatataa tatataatat 420

atatttaata tatttattaa ttatttgtta tatatttatt aatatataat atataatata 480

tttaatatat tataactata tattatatta taattatata tattatatat atacaattat 540

aattatatat tatatatact tataatatat at 572

<210> 15

<211> 357

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(357)

<223> MAR of human chromosome 1, genomic contig; 1842332 to 1842688

<400> 15

tatatctata tatatctata tatatataat atagataata tctatatata taatatagat 60

aatattatct atatataata tagataatat tatctatata taatatagat aatattatct 120

atatataaaa ttatattata tctatatata ttatatatat aaaattatat tatatctata 180

tataatatag ataatatcta tatataaata gataatatct atatatataa tatagatatt 240

atctatatta tagatataga taatattatc tatattatag atattatcta tatataatat 300

agataatatt atctatatta tatatataat atatctatat tatctataat attatct 357

<210> 16

<211> 399

<212> DNA

SEL PCT 012.ST25

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(399)

<223> MAR of human chromosome 1, genomic contig; 2309560 to 2309958

<400> 16
attatatata atatatatta tatattatat atatcaagca gcagatataa tatataatat 60

atataatata tataatatat attgtatatt atataatata taatatatat aatatatatt 120

gtatattata taatatataa tatatataat atatattgta tattatataa tatataatat 180

atataatata tattgtatat tatataatat ataatatatg taatatatta tgtaatatat 240

tatataatat atattatata ttatatataa tatatattat atataatata tattacataa 300

tatattacat atattacgta atatatgtta tatattacat ataatatata acatatatta 360

cgtaatatat gtaatatatt acatataata tatacatta 399

<210> 17

<211> 394

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(394)

<223> MAR of human chromosome 1, genomic contig; 2231759 to 2232152

SEL PCT 012.ST25

<400> 17
atatatactt ataaattata tacttatata tacttataaa ttatatactt atatatactt 60

ataaattata tacttatata tacttataaa ttatatactt atatatactt ataaattata 120

tacttatata tacttataaa ttatatactt atatatactt ataaattata tacttatata 180

tacttataaa ttatatactt atatataatt ataaattata tacttatata taattataaa 240

ttatatactt atatataatt ataaattata tacttatata taattataaa ttatatactt 300

atatataatt ataaattata tacatatata taattataaa ttatatacat atataattat 360

aaattatata catatataat tataaattat atac 394

<210> 18

<211> 387

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(387)

<223> MAR of human chromosome 1, genomic contig; 7406524 to 7406910

<400> 18
tatattatat ataatatata ttatatataa tataaataat atatattata tataatatat 60

aaataatata taatatataa ataatatata atatataata tataaataat atataatata 120

taacatataa ataatatata taatatataa ataatatata taatatataa ataatatata 180

taatatataa aaatatataa tatataatac atatataaat aatatattat attatatatg 240

atacataata tattatatat aatatattat atgatacata atatattata tagaatatat 300

tatatgatac ataatatatt atatagaata tattatatga tacataatat attatatgat 360

acataatata ttatatataa tatatta 387

<210> 19

<211> 370

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(370)

<223> MAR of human chromosome 1, genomic contig; 9399572 to 9399941

<400> 19
catatataca tatatacaca tatatacaca tatatataca catacatatg tacacatata 60

tatacacata tgtatacaca tatatacaca tatatacaca catatataca catatataca 120

cacatatata cacatatata cacatatata cacatataca catatataca catatataca 180

tatatacaca tatatataat atacacacat atatatacac atatatacac acatatatac 240

acatatatac acatatatat acacatatat acacatatat acatatatac acatatatat 300

acatatatac acatatatac atatatacac atatatacat atatacacac atatatacac 360

atacatatac 370

<210> 20

<211> 377

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(377)

<223> MAR of human chromosome 1, genomic contig; 12417411 to 12417787

<400> 20
attatatata atacatataa ttatatattt atatataaat tataataaat acatataatt 60

atatatttat atataaatta tatataataa atacatataa ttacatatat ttataaatta 120

taataaatac atataattac atatatttat atatgaatta tatataataa atacatataa 180

ttatatatat ttatatgtag attatatata aatatatata atttatatat ataataatat 240

atataattta tatatataat tatatatata ataaatatat ataatttata tatataatta 300

tatatataat aaatatataa taatatatat aatttatata tataattata tatataataa 360

atatatataa tttatat 377

<210> 21

<211> 1524

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1524)

<223> MAR of human chromosome 1, genomic contig; 1643307 to 1644830

<400> 21
tataaatata tataaatata taaatatata taaatatata aatatatata aatatatata 60

aatatataaa aatatataaa tatatataaa tatatataaa tatataaaaa cataaaaata 120

SEL PCT 012.ST25

tatataaata tatataaata tataaaaata tataaatata taaatatata aaaatataca 180

aatatataaa tatatacata aatatatata aatatatata aatatataaa aatatatata 240

aatatataaa tatatataaa tatatataaa tatatataaa tatataaaaa tatatataaa 300

tatataaata tataaaaata tatataaata tataaatata taaatatata taaatatata 360

aatatataaa taaatataag tatttatgaa tatatatgaa tatataaata tataaaaaat 420

atatataaat atataaatat atataaatat ataaatatat acatatatac atatataaat 480

aaataaatat aagtatttat gaatatatat gaatatataa atatataaaa aatatatata 540

aatatataaa tatatataaa tataaatata taaaaatata taaaaatata tataaatata 600

taaatatata taaatatata aatatatata aatatatata aatatataaa tatatataaa 660

tatatataaa tatataaata tataaatata tataaatata tataaatata taaatatata 720

aatataaata tataaatata tataaatata tataaatata taaatatata taaatatata 780

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SEL PCT 012.ST25

<211> 664

<212> DNA

<213> Homo sapiens

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<223> MAR of human chromosome 1, genomic contig; 1398763 to 1399426

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atatatacac acatatatat aaaatatata tatacacaca tatatataaa atatatatat 480

acacatatat ataaaatata tatatacaca tatatataaa atatatatat atacacatat 540

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SEL PCT 012.ST25

<213> Homo sapiens

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<223> MAR of human chromosome 2, genomic contig; 17840365 to 17841792

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SEL PCT 012.ST25

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<210> 24

<211> 4624

<212> DNA

<213> Homo sapiens

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SEL PCT 012.ST25

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SEL PCT 012.ST25

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<212> DNA

<213> Homo sapiens

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tgggaattgg aaagacaaat atcgttaaga gaaaattgct tttaggagag gggaaagaat 240

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gactgtgtga aaaaccatca gttctgtcat attcctaaaa aaaaattaaa aagttaaaaa 420

SEL PCT 012.ST25

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SEL PCT 012.ST25

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<210> 28

SEL PCT 012.ST25

<211> 677

<212> DNA

<213> Homo sapiens

<220>

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<222> (1)..(677)

<223> MAR of chromosome 1 genomic contig; 12803267..12803943

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agtatacgta atagtatata tcatatagta tacgtaatag tatatatcat atagtatacg 300

taatagtata tatcatatag tatacgtaat agtatatatc atatagtata cgtaatagta 360

tatatcatat agtatacgta atagtatata tcatatagta tacgtaatag tatatatcat 420

atagtatacg taatagtata tatcatatag tatacgtaat agtatatatc atatagtata 480

tattatatag tatatatcat atagtatata ttatatagta tatatcatat agtatatatt 540

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<210> 29

<211> 332

<212> DNA

<213> Homo sapiens

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<222> (1)..(332)

<223> MAR of chromosome 1 genomic contig; 13079684..13080015

<400> 29
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attatataat tatatattaa tatatattaa ttatattata tatattatat aattatatat 120

taatatatat taattatatt atatatatta tataattata tattaatata tattaattat 180

attatatata ttatatatta taattatata ttatataatt ataatatata tgttaatata 240

atatatataa ttaatatata attaaaacta tttaattata tgtatattat atataatatg 300

tattatttaa ataataaata tattatttat at 332

<210> 30

<211> 479

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(479)

<223> MAr of chromosome 1 genomic contig; 15682296..15682774

<400> 30

SEL PCT 012.ST25

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acaagtacat atatatagta tatatatata tacaagtaca tatatatagt atatatatat 120

acaagtacat atatatagta tatatatata caagtacata tatatatagt atatatatat 180

acaagtacat atatatagta tatatatata caagtacata tatatatagt atatatatat 240

acaagtacat atatatagta tatatatata caagtacata tatatatagt atatatatat 300

acaagtacat atatatatag tatatatata tacaagtaca tatatatata gtatatatat 360

atacaagtac atatatatag tatatataca tatatacaag tacatatata tagtgtatat 420

atatatatac aagtacatat atatacttgt attagtatat atatatatat atacaagta 479

<210> 31

<211> 531

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(531)

<223> MAr of chromosome 1 genomic contig; 15694611..15695141

<400> 31

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cataataata tataatgaat ataatataaa ataaatataa taaaatatat aatatatcta 120

ttatgtatta tatattatat atgtttatat ataatataat tatatatgtt tatatataat 180

ataattatat atgtttatat ataatataat tatatattat atattataga tataatatat 240

aatatactat atattataga tataatatat aatatactat atattataga tataatatat 300

aatatactat atattataga tataatatat aatatactat atattataga tataatatat 360

aatatactat atattataga tataatatat aatatatatt atatattata gatataatat 420

ataatatatt atatattata tctatatata atatattgta tattatatat aatatattgt 480

atattatata taatatattg tatattatat ataatatatt gtatattata t 531

<210> 32

<211> 378

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(378)

<223> MAR of chromosome 1 genomic contig; 886276..886653

<400> 32
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attatataca atataattta tatataaaat ataaattata taaataattt atatataaaa 120

tataaattat ataaataatt tatatataaa atataaatta tgtataaaat ttatatataa 180

aatataaatt gtgtataaaa ttatatataa aatataaatt gtgtataaaa tttatatata 240

aaatataaat tatatataat ttatatatta taatataaat tatatataat atatatcata 300

aaatataaat tatatataat atatatcata agatataaat tatatataat atatatcata 360

agatataaaa tatataat 378

<210> 33

<211> 595

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(595)

<223> MAR of chromosome 1 genomic contig; 3326732..3327326

<400> 33
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aatatatata aatatatata aaaatatata aatatatata aatatatata aaatatataa 120

atatatataa aatatatata aatatatata aatatatata aaaatataaa tatatataaa 180

aatataaata tatataaata tatataaaaa tataaatata tataaatata tataaatata 240

taaatatata taaatatata taaatatata aatatatata aatatatata aatatatata 300

aatatataaa tatataaaaa tatatataaa tatataaata tatataaata tataaatata 360

taaaaatata tataaatata taaatatata taaatatata taaatatata tataaatata 420

tataaatata tatatatata aatatatata aatatatata taaatatata taaatatata 480

tatatatata taaatatata taaatatata taaatatata tataaatata tataaatata 540

tataaatata tatataaata tatataaata tatatataaa tatatataaa tatat 595

<210> 34

<211> 738

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(738)

SEL PCT 012.ST25

<223> MAR of chromosome 1 genomic contig; 4485716..4486453

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ttgtatataa tatatatcat attatattgt atataatata tatcatatta tattgtatat 240

aatatatatc atattatatt gtatataata tatatcatat tatattgtat ataatatata 300

tcatattata ttgtatataa tatatatcat attatattgt atataatata tatcatatta 360

tattgtatat aatatatatc atattatatt gtatataata tatatcatat tatattgtat 420

ataatatata tcatattata ttgtatataa tatatatcat attatattgt atataatata 480

tatcatatta tattgtatat aatatatatc atatattatc tattatattg tatataatat 540

atattatata ttatctatta tattgtatat aatatatatt atatattatc tattatattg 600

tatataatat atattatata ttatctatta tattgtatat aatatataat aaatatagta 660

tatataatag ataatatata gtatatatga tatattatat atactatata ttatatatca 720

tatatactat atactata 738

<210> 35

<211> 386

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(386)

<223> MAR of chromosome 1 genomic contig; 5423067..5423452

<400> 35
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tatataaata tataaatata taaatatata tttatataaa tatataaata tataaatata 120

taaatatata tttatataaa tatataaata tatatttata taaatatata aatatatata 180

aaatatataa atatatattt atataaatat ataaatatat ataaaatata taaatatata 240

tattttatat aaatatataa atatatataa aatatataaa tatatatatt ttatataaat 300

atataaatat atataaaata tataaatata tatattttat atatttatat atataaatac 360

atatatttca tatatcacat atatga 386

<210> 36

<211> 584

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(584)

<223> MAR of chromosome 1 genomic contig; 5805559..5806142

<400> 36
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atatatatta taatataata tatataatac tgtatattat attatatata ttataatata 120

tattattata tattatatta tatataatat aatatatatt ataatatatt atattataca 180

tattataatg tattataata tatattatat tatatattat aatatatatt atattatata 240

ttataatata tattatatta tatattataa tatatattat attatattat atatattata 300

atacatatta taatacatat tatataatat attataatat gtattataat acatattata 360

taatatatta taatatatta tatataataa tatattataa tacatattat atataatata 420

tattatgtat attatatata atatatatta caatgtatat tatgtatatt atatatatta 480

tatatcatat aatatatatt atatataata tgatatataa tatatattat ataatatatt 540

atatgatata tataatatgt attacatgta atatatatca taat 584

<210> 37

<211> 345

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(345)

<223> MAR of chromosome 1 genomic contig; 10802644..10802988

<400> 37

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atatatatag tgtatatata tactatatat atagtatata gtatatatag taatatatat 120

atatagtata tatatacact atatatagta tatatagtat atatatattg tgtatatagt 180

atatatatag tgtatatata gtatatatat attgtatata tagtatatat attgtgtata 240

tatagtatat atatagtata tatagtatat atagtatata tatagtatat atatactata 300

tatatagtat atatatattg tatatatata ctatatatat agtat 345

<210> 38

<211> 474

<212> DNA

SEL PCT 012.ST25

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(474)

<223> MAR of chromosome 1 genomic contig; 13496468..13496941

<400> 38
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ctataattat atattatata taatatatat tatatataat atataattat atataattta 120

tataatataa tatataatat ataattatat ataattatat aatataatat ataatatata 180

attatatata atttatataa tataatatat aatatataat tatatatatt tatataatat 240

aattatatat aatatataat tatatataat ttatataata taattatata taatatataa 300

ttatatataa tttatataat ataattatat ataattatat attatatata atttatataa 360

tataattata tataatatat aattatatat aatatataat tatatataat tatatataat 420

atataattat atataattta tataatataa ttatatatta tatatattat atat 474

<210> 39

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(483)

<223> MAR of chromosome 1 genomic contig; 2509163..2509645

SEL PCT 012.ST25

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ctattataat atataaacta tataatatat actattataa tatatgaact attataatat 180

ataaactata tataatatat aatatgtact attataatat ataaactatt ataatataat 240

atataaacta ttataataca taaactatta taatatatat aatactatgt atacatatat 300

tacattatgt acatactaca ttatgtatta tgtatgtata tatacacaaa atacataata 360

tataatagta ttatataata gtatatatag ttataatata tagtataatt acaatatata 420

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cta 483

<210> 40

<211> 641

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(641)

<223> MAR of chromosome 1 genomic contig; 2776349..2776989

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atgttatata taacatagat attatatata catgttatat ataacagata ttatatatac 180

atgttatata taacatagat attatatatg tatgttatat ataacataga tattatatat 240

gtttatataa tatataacat atgtttaaca tatataatat ataacatgtt tatataatat 300

ataacataat tatatgttat atatgatata aaacatatat attatatacg ttatatgtaa 360

tatataacat atattgtata cgttatatgt aatatataac atatattgta tacgttatat 420

gtaatatata acatatattg tatacgttat atgtaatata taacatatat tgcatacgtt 480

atatgtaata tataacatat attgtatacg ttatatgtaa tatgtaacat atattgtata 540

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taacatatat ataacatata taacatatat gttatattat a 641

<210> 41

<211> 745

<212> DNA

<213> Homo sapiens

<220>

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<222> (1)..(745)

<223> MAR of chromosome 1 genomic contig; 2858703..2859447

<400> 41

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tatataataa aatatgtaat aatatataat atatttatat ataaatatat tatattatat 120

atatattatt atatttataa tataatatat atttatatta tatattataa atatatatta 180

tataatatat attataaata tatattatat aatatatatt ataaatatat attatattat 240

atattataaa tatatattat ataatatata ttataaatat atattatata atatatatta 300

taaatatata ttatatttat aatatatatt tttgtatatt atatattata tattataaat 360

SEL PCT 012.ST25

attattatat ttataatata ttatatattt tatatataat atatgatata tattataaat 420

atatcttata aatatatata tttatatata tatattataa atatataaat ataaatatat 480

aatataatat aatataatat aataaatata atatataata tatataatat ataataaata 540

taataaatat aaatatatca tataaatata aatataaata taaatatatc atataaatat 600

atatatttat atgatatatt atagtatata taaatatatt tatatattat aaaatattta 660

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<210> 42

<211> 307

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(307)

<223> MAR of chromosome 1 genomic contig; 945522..945828

<400> 42

catatataat atatattacc tatgttatat aggtcatata taacataaat atattacata 60

tatgtaatat atattaaata taaatatata acatatatgt gtaactatat atgtaaatat 120

gtacatatac atatatgtaa atatataata tatatttaca ttatattata taatatatat 180

ttacattata tatttatata tacattatat atatttacat tataaatatt tatataatat 240

atatttacat tatattacat tatataaaat acaatatatt acattataat acattataac 300

agataaa 307

<210> 43

SEL PCT 012.ST25

<211> 357

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(357)

<223> MAR of chromosome 1 genomic contig; 3402743..3403099

<400> 43
aatattatat taaatataat atattaatat ttaatatatt taatataata ttaaataaat 60

atattataaa taaattataa tatataaata tatattatgt atttatgtat aatatataaa 120

aattatatat aatatatata tttttataaa tatataaata tataataaat aaatatatta 180

aataaataat aatatattaa atattaatat attaaatatt atatattaaa tataatatgt 240

aatatgaaat atattaaata ttatatatta aatataatat ataatgtgaa atatattaaa 300

tattatatat taaatataat atataatatg aaatatatta aatattatat attaaat 357

<210> 44

<211> 323

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(323)

<223> MAR of chromosome 1 genomic contig; 3485830..3486152

<400> 44
atatttatag actatatatt tatatattta gtgtatttgt atactatata tttatatagt 60

tagtatattt gtatactata tatttatata tttagtatat ttgtatacta tatatttata 120

tatttagaat atttgtatac tatatattta tatatttagt atatttgtat actatatatt 180

tagtatattt gtatactata tatttatata tttagtatat ttgtatacta tatatttata 240

tatttagtat atttatatac tatatactta tatatttagt atatttatat actatatact 300

tatatattta gtatatttat ata 323

<210> 45

<211> 498

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(498)

<223> MAR of chromosome 1 genomic contig; 3548336..3548833

<400> 45
aattattact atattgttaa tataattatt atataatata atataattat atcactatta 60

ttatattata gtattaatat aatagtgtat aacattaata taatatagta ttaatataat 120

agcgtataac attaatataa tatagtatta atataatagc gtataacatt aatataatat 180

agtattaata taatagtgta tattaatata atatagtatt aatatataat attaatataa 240

tatatcaata taatagtata taatataata taatatatca atataatagt atataatata 300

atataatata tcaatataat agtatataat ataatataat atatcaatat aatagtatat 360

aatattaata taatataata tcaatataat agtatataat attaatatat taatataata 420

gtatataata ttaatgtaat ataatattaa cataatgtat ataataatat aatagtatat 480

aatactaata taatataa 498

<210> 46

<211> 400

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(400)

<223> MAr of chromosome 1 genomic contig; 4595109..4595508

<400> 46

aaatatatta tattatatat tatatattat tcaatatact ataatatata ttatatatgt 60

ttaatacaat atataatatt tacatatatt cccatttatt tatataacat atattatatg 120

atattatata ttactccata taatataata tattatacat aatatattac tcagtataat 180

acataatata tataatatat tactcggtat aatatataat attatatgtt atgcaatata 240

atatataata ttatatataa tacattattc aatataatat ataatattat atataataca 300

ttattcaata taatatataa tacactattc aatataatat acaatattat atataataca 360

ttattcaata taatatatat tatataatat atatatttat 400

<210> 47

<211> 403

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(403)

<223> MAr of chromosome 1 genomic contig; 7205509..7205911

<400> 47
agtatatata tgtgtatata tatgagtata tatatgtgta tatatatgag tatatatatg 60

tgtatatata tgagtatata tatgtgtata tatatgagta tatatatgtg tatatatatg 120

agtatatata tgtgtatata tatgagtata tatatgtgta tatatatgag tatatatatg 180

tgtatatata tgagtatata tatgtgtata tatgagtata tatatgtgta tatatgagta 240

tatatatatg tgtatatatg tgagtatata tatgtgtata tatatgagta tatatgtgta 300

tatatatgag tatacatatg tgtatatata tgagcatata tgtgtatata tatgagtata 360

tatatgtgta tatatatgag tatatatgtg tatatatatg agt 403

<210> 48

<211> 309

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(309)

<223> MAR of chromosome 1 genomic contig; 7507280..7507588

<400> 48

SEL PCT 012.ST25

tataaaatat atattattta tatattatat ataaaatata tattatatta tatattatag 60

atataataaa taaataatat ataatatatt atataattat ttatacataa ttatatataa 120

ttatatgtaa ttgtacaatt atatataatt atatacaatt atacacataa ttatatacaa 180

ttatacaatt atatacataa ttatatatat aatatacata attatatatt aattatacaa 240

ttatatacat aattatatat aattatacaa ttatatacat aattattatg tatattatat 300

tatataata 309

<210> 49

<211> 516

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(516)

<223> MAR of chromosome 1 genomic contig; 3581085..3581600

<400> 49

atatatatat atatatatat atttatatat atatatatta atatatatta tataaaaaa 60

tatataaaat ttatatatat aatttatata tataaaaata tataaaattt atatatataa 120

tttatatata taaaaatata taaaatttat atatataatt tatatatata aaaatatata 180

aaatttatat atataattta tatatataaa aatatataaa atttatatat ataatttata 240

tatataaaaa tatataaaat ttatatatat aatttatata tataaaaata tataaattt 300

atatatataa tttatatata taaaatatat aaattatata tataattata tatataatat 360

aaaattatat atataattat atatataata taaaattata tatataatta tatatataat 420

ataaaattat atatatattg tatatatata aaatatacaa aatttatata tataaaatat 480

aaaatataca taaaaataaa tatatataat ttatat 516

<210> 50

<211> 534

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(534)

<223> MAR of chromosome 1 genomic contig; 3084851..3085384

<400> 50
atataaatata tatgactata tattttatat tatattctat ttcaataaaa tatttatatt 60

ttattatata ttataatata taattatata tgtaataata tataatatat aatatatatt 120

ttatattata ttttatattt atttttatat tttatattat atttattat atatattata 180

atatataatt atatatgcaa taatatatta tatattataa tatataatta tatatgcaat 240

aatatattat atattataat atataattat atatgcaata atatattata gattataata 300

tataattata tatgcaataa tatattatat attatatatt agataatata ttaatatata 360

ttataacata taatatataa catataatat ataatatatt atctaatata taatataaca 420

tataatatat aatatattat ataatatatt attacatata taatatattg taatatataa 480

tattacatat atcttcaaaa agagttatgt gtatataata catatatata ccat 534

<210> 51

<211> 583

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(583)

<223> MAR of chromosome 1 genomic contig; 160087..160669

<400> 51
tatttatata aaatatataa aatatattat atataaatat attatatata atatatttat 60

atattataca atatatttat atattatata taatatattt tatataatat acataatata 120

ttttatatat tatatataat atattttata tataatgtac aatatatttt atatattata 180

tataatatat tttatatata ctatacaata tattttatat attatatatt ttatatatat 240

ttttcatgta acatatatat tttatatata atatatatac catatataat atattttata 300

tataatatat ataccatata taatatattt tatatataat atgtatatca tatatagtat 360

attttatata taataggtat accatatata atatatttta tatataatag gtataacata 420

tataatatat tttatatata atatgtatac catatataat atattttata tattatagat 480

accatatgta atatacttta tatataatat agataccata tgtaatatac tttatatata 540

atatagatac catatgtaat atactttata tataatatag ata 583

<210> 52

<211> 314

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(314)

SEL PCT 012.ST25

<223> MAR of chromosome 1 genomic contig; 4350424..4350737

<400> 52
tatgtgtata taaatatatg tatatatgtg tatataaata tatataaata tatgtatata 60

tgtatatata catatattta tatataaata tatgcatata tttatatata aaatatatgc 120

atatatgtat atatataaaa tatatacata tatgtatata tataaaatat atacatatat 180

gtatatatat aaaatatata catatatgta tatatataaa atatatacat atatgtatat 240

atataaaata tatacatata tgtatatata taaaatatat acatatattt atatatataa 300

aataccaagt ctta 314

<210> 53

<211> 828

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(828)

<223> MAR of chromosome 1 genomic contig; 8443267..8444094

<400> 53
tattatataa ttatatatac tatataatta tataatatat agttatatag tatatataat 60

atatataata tatactatag tatatataat atatataata tatactatag tatatataat 120

atataattat atataatata tataatatag tatatattat atatatatta tatatatata 180

atatatatat aatatatata atatagtata tataatatat aattatatat aatatataat 240

atagtatata taatatataa tatatatata attatatact ataatatata taatatataa 300

SEL PCT 012.ST25

ttatatatta tatactatag tatatattat tatatataat agatataata tatataatta 360

ttatataata tagtatatat aatatataat tatatataat agatataata taatataatt 420

atatataata tagtatatat aatatataat tatattatat tatatataat atataattat 480

aatatataat tatattatat aatatatata atatataatt atattatata attatattat 540

ataatatata taatatataa ttatattata taatatatat aatatataat tatattatat 600

aatatatata atatataatt atattatata atatatataa tatataatta tattatataa 660

tatatataat atataattat atattatata taatatagta tatataatat gtaattatat 720

atcatataat atataacatt gtatataata tataattaca tattatataa tgtatataat 780

atataattat atacattata taatatagta tataattata tattatgt 828

<210> 54

<211> 573

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(573)

<223> MAR of chromosome 1 genomic contig; 8703190..8703762

<400> 54

tatattatat ataaaatata catataatat acctataata tacatataat atataatata 60

tattatgtac atataatata catataatat atataatata taatgtacat ataatataca 120

tataatatat gttatatatt atatataaaa tataggatat atataatata gaatatatat 180

actatattgt atatataaga tatataatat atagtatata tactatataa tatataatat 240

atagtatata taatatataa tatagaatat atatacaata tataatatag aatataggat 300

SEL PCT 012.ST25

atatatagaa tatacatata taatatgtat atattatata ttatattata tattatataa 360

aaatatataa tatataatat aaaaatatat tatatattat ataatataaa atatattata 420

tattatatat tatataatat aaaatatatt atatattata tattatatat aaaatatatt 480

atatattata tattatatat aaaaatatat tatatattat atattatata taaaaatata 540

ttatatatta tatataaaaa tatatattat tac 573

<210> 55

<211> 597

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(597)

<223> MAR of chromosome 1 genomic contig; 8819076..8819672

<400> 55

acatatctta tataaaaat atataaatat acacatattt tatatataat atatattata 60

tatatgaaat atacacatat ttttatatat ataatatata tattatatat aatatatgca 120

tatattatat ataaaatata tatattatat ataaaatatg catatattat atataatata 180

tataatataa aatatataat atatattata tattatatat aatatatatt atatataata 240

catatatata atatataata tatataaaat ataatatata tattatataa tatatatata 300

aatatatata atatatatat aatatatata ttatatataa aatatatatt atatgtaaaa 360

tatataatat atataatata tatattatat gtaaaatata tattatatat aaaatatata 420

atatataaaa tatatattat atataaaata tataatatat aaaatatata atatatataa 480

aatatataat atatataaat atatattata tataaaatat ataatatata taaatatata 540

SEL PCT 012.ST25

ttatatataa aatatataat atatataaat atatattata tataaaatat atattat 597

<210> 56

<211> 646

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(646)

<223> MAr of chromosome 1 genomic contig; 759619..760264

<400> 56

taatatatat aatatatatt atataataat atataatata tattatatta taatatataa 60

tatattatat aataatatat attatataat atataataat atatataata catattattt 120

aataatatat aatatatatt atataataat atataatata tattatataa taatatacat 180

tatattatat aatatataat atatataata tatattatat aataatatat aatatatatt 240

atagaatgat atattagata ttatataatt atatatataa tattatatat tatataataa 300

tatataatat atattatata attatatata taatattata tattatataa ttatatataa 360

tatattatat aattatatat ataatattat atattatata attatatata atatatatta 420

tataattata tatataatac tatatattat ataattatat ataatactat atattatata 480

atttatataa ttatatatat tatatattat ataattatat atattatata ttatataata 540

acatatatat tatatattat ataataacat atatattata tattatataa tacatatata 600

ttatatatta tataatacat tattatataa tatataatat atatta 646

<210> 57

<211> 752

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(752)

<223> MAR of chromosome 1 genomic contig; 1226710..1227461

<400> 57
taaacatata tataaatata tataaatata tatataaata tatataaata tataaatata 60

taaatatata tgaatatata aatatatata aatatatatg aatatataaa tatatatata 120

aatatatata aatatatata taaatatata taaatatata taaatatata taaatatata 180

taaataaata tataaatata tataaatata taaatatata tataaatatg taaataaata 240

tatataaata tataaatata tataaatata tataaatata tatagaaata tatatagaaa 300

tatatataaa tatatataga aatatataga aatatatata gaaatatata taaatatata 360

taaatataga aatatatata aatatatata aatatatata gaaatatata atatatataa 420

atatatataa atatataaat atatatataa atatatatat aaatatatat aaatatatat 480

aaatatatat aaatatatat aaatatatat attaatatat aaatctatat taatatatat 540

taatatataa atctatatta atatatatta atatatatat taatatatat taatatataa 600

atatatatat taatatataa atatatataa atatatatgt aaatatatat ataaatatat 660

ataaatatat atataaatac atataaatat atatataaat atatataaat atatatataa 720

atatatataa atatatatat aaatatatat aa 752

<210> 58

<211> 300

<212> DNA

SEL PCT 012.ST25

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(300)

<223> MAR of chromosome 1 genomic contig; 1119049..1119348

<400> 58
taatatacat tttatataat atatgtaata tatattttat atatatgtaa tatatatttt 60

atataatata tgtaatatat attttatata tatgtaatat atattttata taatatatgt 120

aatatatatt ttatataata tatgtaatat atattttata taatatatgt aatatatatt 180

ttatataata tatgtaatat atattttata taatatatgt aatatatatt ttatataata 240

tatgtaatat atattttata taatatatgt aatatatatt ttatatatat gtaatacata 300

<210> 59

<211> 617

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(617)

<223> MAR of chromosome 1 genomic contig; 3603613..3604229

<400> 59
aaaatataat atatataata tataatatat ataatatatt atatataaaa tatataatat 60

SEL PCT 012.ST25

ataatatata taataaaata tacataatat ataatgtata ataaaatata cataatatat 120

aatatataat aaatatataa tatataatat ataataaaat atataatata taatatataa 180

taaaatatat aatatattat atataataaa atatataata tattatatat aataaaatat 240

ataatatatt atatataata aaatatataa tatattatat ataataaaat atataatata 300

ttatatataa taaaatatat aatatattat atataataaa atatataata tataatatat 360

aataatatat ataatatata atatatataa taaaatatat ataatatata atatatataa 420

taaaatatat aatatataat atatataata aaatatatat gatatataat atatataata 480

aaatatatga tatataatat atataataaa atatataata tataatataa tatataatat 540

atatactaaa aaatatataa tatataataa aaaatatata atatataata tatataatat 600

ataataaaat atatata 617

<210> 60

<211> 674

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(674)

<223> MAR of chromosome 1 genomic contig; 2592460..2593133

<400> 60

taagcttata tatatatata agcttatata tatatatata agcttatata tatatagaaa 60

gcttatatat atatagaaag cttatatata taagaagctt atatataaaa gcttatgtat 120

aaatatatat aaatatattt atttatgctt atagatacat atataaatat atttatttat 180

atttatatat aaacatatat ttatatatat ttatataata tttatttatt atataaataa 240

atatataata aataataaat atatataata tatttattgt attatttata taaatttatt 300

aatataatat ataataaaat aataattata taaatatata aatatctata aatatatata 360

aatatatata atatctataa atatatataa atataaatat atataatatc tataaatata 420

gataaatata aatatatata atatctataa atatagataa atataaatat atataactat 480

atataaatat atataactat atataaatat atatataaat atatataact atatatataa 540

ctatatatat aaatatatat aactatatat ataaatatat atataaatat atataactat 600

atatataaat atatataact atatataaat atatatataa atatatataa ctatatatat 660

aaatatatat ataa 674

<210> 61

<211> 1694

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1694)

<223> MAR of chromosome 1 genomic contig; 2891680..2893373

<400> 61

atatgtaata catatattat atatgcatat atacatgcat atgtatatac atatattata 60

tatgcatata tacatgcata tgtatataca tatataaagt atgattatat ataatatata 120

catgtatatg tatatacatg tatatattat attatatatt atttatacat attattatgt 180

ctatatataa tataatatat acatattaat aatataatac ataatataat ataatatatt 240

atataataca taatataata taatatatta tataatacat aatataatat aatatattat 300

atgatacata atataatata atatattata tgatacataa tataatataa tacatattaa 360

SEL PCT 012.ST25

taatatatta ttattattaa tataatatat acatattaat atacatacat atatattata 420

ttatatataa tatacatata atataatatg taatattata tataatataa tacataatat 480

aatacatatt aataatatat tattaataag ataatatata tgtatctata atatatacat 540

atatgtatat gtatgtatat attatagata tacatgttta tacatgtata tattatagat 600

atatacatgt atatacatgt atatattata gatatataca tgtatatacg tatatattat 660

agatatacat gtatatatgt atatatatta tagatataat atatacaaga atataagaat 720

atatataata taatatataa tacacataat acgtatatat tatatataca tgtatattat 780

atatgtacat atatacatgt atattatata tacatgtata ttatatatac atgcatatta 840

tatatatttt tatatataat atccatgtat attatgtata tttgtgtata ttatatatac 900

atgtatatta tatatacatg catattatat atatttttat atataatatc catatatatt 960

atgtatattt gtgtatatta tatatacaca tatattatat atacatggat attatatata 1020

cacatatatt atatatacat atatattata tatacacata tattatatat acatgtatat 1080

tatatataca cgtatattat atatacacac gtatattata tatacacgta tattatatat 1140

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tatattatat atacacacgt atattatata tacacgtata ttatatatac acacgtatat 1260

tatatataca cgtatattat atatacacac gtatattata tatacacgta tattatatat 1320

acacacgtat attatatata cacgtatatt atatatacac acgtatatta tatatacatg 1380

tatattatat atacatgtat attatatata cacatgtata ttatatatac atgtatatta 1440

tatatacaca tgtatattat atatgcatgt atattatata tacacatgta tattatatat 1500

acacatgtat attatatata catatatatt atatatacat gtatattatg tatacatata 1560

tattatatat acatgtatat tatagataca tatatattaa atatacatgt atattatgta 1620

tacatatata ttaaatatac atgtatattg tatatacata tatattatat acatgtatat 1680

tacatgtata cata 1694

<210> 62

<211> 587

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(587)

<223> MAR of chromosome 1 genomic contig; 3432560..3433146

<400> 62
gaattatata tatatagctg aattatatac atatataata tatacaatat atattatata 60

tttatatatg atatatacaa tatatattac atattatata tacaatatat aatatataat 120

atataatatt atatattata tattgtatat aatatatatt atataacatt atataatata 180

taatattata tattatatat tgtatataat atatattata taacattata taatatatac 240

tattatatat tataatatat aatatataat aatatataat agtatatatt atatatattg 300

tatatattat atataaatat ataatatata atatatatta tataatatat attatataat 360

atatattatt atatattata tatttatata taatatatat tatatatatt atattttata 420

tataaatata taatatataa taatatataa tttaatatat ataatatata caatatataa 480

tatataatat attaatatat ataatatata caatatataa tatataatat ataatatata 540

atataaatta ttatatataa tatatattat atatagctga attatat 587

<210> 63

<211> 313

<212> DNA

<213> Homo sapiens

<220>

SEL PCT 012.ST25

<221> misc_binding

<222> (1)..(313)

<223> MAR of chromosome 1 genomic contig; 3805392..3805704

<400> 63
tatataatat gtatattatg taatatttta tatagcatat atgtatatta tatataatct 60

tttatatata gtatataata tgtatattat atattatata attatataat tatgtattat 120

ataaaatata ttatataata tataattata tatttttga aatatagatt atatataata 180

tatatggcag tgagctgaga tataatatat attatctata ctatataata tatattatat 240

atactctata ttatatatgt atatattata tataatatat acatatataa tgtgtatata 300

ttatatataa taa 313

<210> 64

<211> 349

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(349)

<223> MAR of chromosome 1 genomic contig; 4521378..4521726

<400> 64
ttatatacac tatataatat gtatttatat atacttatat acactatata tgtatttata 60

tataattata tacactatat aatatgtatt tatatataat tatatacact atataatatg 120

tatttatata taattatata cactatataa tatgtattta tatataattg tatacactat 180

SEL PCT 012.ST25

ataatgtata tttatatata attgtataca ctatataatg tatatttatg tataattgta 240

tacactatat aatgtatatt tatgtataat tgtatacact atataatgta tatttatgta 300

taattgtata taccatataa tgtatattta tgtataattg tatatacca 349

<210> 65

<211> 500

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(500)

<223> MAR of chromosome 1 genomic contig; 3240166..3240665

<400> 65

ttaatatata atatatatta tatatttata tattaatata taatatatat ttatatataa 60

tatatattat atatttatat tacatatatt tatatgttaa tatatatttt atatatttat 120

atattttata tatttatata ttatatattt atatattata tttatatatt atatatttat 180

attatatatt tatatattat atttatatat tatatattta tattatatat ttatatattg 240

tatatttata ttatatattt atatattgta tttatatatt atatatttat atactatata 300

tatttatata tattatatat ttatatatta tatatattta tatatattat atatttatat 360

attatatata tttatatata ttatatattt atatattata tatatttata tatattatat 420

atatttatat atattatata tttatatata atatatatta tatattttat ctatatattt 480

atatattaat atatattata 500

<210> 66

<211> 866

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(866)

<223> MAR of chromosome 1 genomic contig; 409429..410294

<400> 66

atatatataa tatattatat atattatata ttatatatat aatacatata ttatatatat 60

aatatataat acatatatta tatatattat atattatata taatatataa tacatatatt 120

atatataata tataatatat aatatattat ataatataat tatataatta tataatataa 180

tataatatat aatattatat aattatataa tatatataat tatattatat attataaata 240

ttatataata tatatattac aaatatatat tatatatatt ataaatatta tataacatat 300

atattatata atatatataa tatataatat atataaaaat ataatatata agatatatat 360

aatatatgat atatatgata tataatatat gatatatatg atatatataa tatatgatat 420

atatgatata tatgatatat ataatatatg atatatatga tatatatgat atatgatata 480

tatgatatat gatatatatg atatatatga tatatgatat atatgatata tatgatatat 540

gatatatatg atatatatga tatatgatat gatatatata atatatgata tgatatatat 600

aatatatgat atatatgata tatgatatgt aatatatatg atatattata tataatatat 660

aatatataca taatatataa tatataatat ataatatata taatatgtga tatatataat 720

atatgatata tgatatatga tatatattat ataatatata taatatatat tatatataat 780

atatattata taatatatat aatatatatt atatataata tataagatat aagatataat 840

atatataata tataatatat ataata 866

<210> 67

SEL PCT 012.ST25

<211> 335

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(335)

<223> MAR of chromosome 1 genomic contig; 614754..615088

<400> 67
acccaatata tgtgtatata tgtatgtata tatacatata catacataca tatatgtaca 60

tacatatata catacataca tatatatgta catacatata tacatacata catatataca 120

tataacatat atacacacat atatacagat atacatatat acatacatat atacatataa 180

catatataca tacatatata catataacac atacatacat acatatatac atacaacata 240

tatacataca tatatacata tgtatacata catatatgta tacatatatg tatacatata 300

tgtatacata tatgtatata tatattgtta tatat 335

<210> 68

<211> 455

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(455)

<223> MAR of chromosome 1 genomic contig; 1299520..1299974

<400> 68
ggatatatat attattagtt gttatattat tatatattat atatattatt atatataata 60

tattatatca tatatattat tatatataat atattatatc atatatatta ttatataata 120

tattatatca tatatattat tatatataat atatattata tatattatta tatataatat 180

atattatata tattattatg tataatatat atattatata ttatttatat atatataaat 240

tatataataa tatataatta attatacata tatacatata taagtataca tataatatat 300

ttatatagta tatataaata tatatacaat atatttatat attatatatt atatataaat 360

atatacaata tatttatatc atatatttta tatatgatac atataatata tattatatat 420

gatatataat atatatcata tatgatatat aacat 455

<210> 69

<211> 404

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(404)

<223> MAR of chromosome 1 genomic contig; 1970778..1971181

<400> 69
atatataata tgtataatat ataatatata tcatatattg ttctatgtat attacatata 60

atatgcatta tatattatat attgcatata atatgcatta tatattatat attgcatata 120

atatgcatta tatattatat attgcatata atatgcatta tatattatat attgcatata 180

atatgcatta tatattatat attgcatata atatgcatta tatattatat attgcatata 240

atatgcatta tatattatat aatatataca catataatat atataattta tatatattta 300

tatatattta catttattat atatttatta tatataaata tatttttata tattacttat 360

atattatata taatatatat aatatatata ttatatataa tata 404

<210> 70

<211> 605

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(605)

<223> MAR of chromosome 1 genomic contig; 3562918..3563522

<400> 70

tatatatata aaatacatat atattatata tattatatat aatacatata ttatatatta 60

tataataatac acgtatataa tatataatat ataatacata taatatatat gatatataat 120

acatataata tatatgatat ataatacata tataatatat atgatatata atacatatat 180

aatatatatt atatataata catatataat atatattata tataatacat atataatata 240

tattatatat aatacatata taatatatat tatatataat acatatataa tatatattat 300

ataatacata tataatatat attatataat acatgtatat aatatatatt atatataata 360

catatatatt atataataca tgtatataat atatattata tataatacat atatattata 420

tattatatat taatatattt atataatagt aatatataat attaatatat tatatatatt 480

aatattatat ataatacata tattatatat aatataaata tatataatac atatataata 540

cacatattat atataataca tatattatat ataatatata tattatatat aatatatatg 600

taata 605

SEL PCT 012.ST25

<210> 71

<211> 317

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(317)

<223> MAR of chromosome 1 genomic contig; 189743..190059

<400> 71
tatttttat atttatatat tatatatatt tttatatgta atatattata tataaaatta 60

tataatttta ctacatataa tatataaaat tatataattt tactacatat aatatataaa 120

attatataat tttactatat ataatatata aaattatata attttatata taatatatat 180

tataatatat attatatgca atatatatta tatattatat tataatatat tgtatatttt 240

tgtatataaa atatataata tataatatat ttatagacaa taatatataa tataatatat 300

aaaattttat atataaa 317

<210> 72

<211> 522

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(522)

SEL PCT 012.ST25

<223> MAR of chromosome 1 genomic contig; 229111..229632

<400> 72
gatatatata tttatatata taaaagatat atattattta tatataaaga tatatattta 60

tatatataaa agatatatat tatttatata tataaaagat atatatttat atatatgata 120

tatattattt atatatataa aagatatata tttatatata tgatatatat tatttatata 180

taaaagatat atataaaaga tatatattat ttatatatat aaaagatata tatataaaag 240

atatatatta tttatatata taaatgatat atattattta tatataaaag atatatatta 300

tttatatata aaagatatat attatttata tatataaaag atatacatat aaaagatata 360

tatttatata taaaagatat atatatttat atataaaaga tacatatatt tatatatata 420

aaagatatat atatttttat atataaaata tatattatat atataaaaga tatatataaa 480

tatatatatc ttttatatat aaaagatata tataaatata ta 522

<210> 73

<211> 1110

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1110)

<223> MAR of chromosome 1 genomic contig; 1138030..1139139

<400> 73
tatgtatgta tacataatat attatatatg tatattatgt atacataata tattatatat 60

gtatattatg tatacataat atattatata tgtatattat gtatacataa tatattatat 120

SEL PCT 012.ST25

attatatgta tattatgtat acataatata ttatatatta tatgtatatt atgtatacat 180

aatatattat atattatatg tatattatgt atacataata tattatatat tatatgtata 240

ttatgtatac ataatatatt atatattata tgtatattat gtatacataa tatattatat 300

attatatgta tattatgtat acataatata ttatatatta tatgtatatt atgtatacat 360

aatatattat atattatatg tatattatgt atacataata tattatatat tatatgtata 420

ttatgtatac ataatatatt atatattata tgtatattat gtatacataa tatattatat 480

attatatgta tattatgtat acataatatt tatatattat atgtatatta tgtatacata 540

atatattata tattatatgt atattatgta tacataatat gtacacataa tatttatata 600

ttatatgtat attatgtata cataatattt atatattata tgtatattat gtatacataa 660

tatttatata ttatatgtat attatgtata cataatattt atatattata tgtatattat 720

gtatacataa tatttatata ttatatgtat attatgtata cataatatat tatatattat 780

atgtatatta tgtatacata atatattata tattatatgt atattatgta tacataatat 840

attatatatt atatgtatat tatgtataca taatatttat atattatatg tatattatgt 900

atacataata tattatatat tatatgtata ttatgtatac ataatatatt atatattata 960

tgtatattat gtatacataa tatattatat attatatatg tatattatgt atacataata 1020

tattatatat tatatatgta tattatgtat tatattatat attatgtata ttatagatta 1080

tgtatgcata cataatatgt attgtatatt 1110

<210> 74

<211> 521

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(521)

<223> MAR of chromosome 1 genomic contig; 2863407..2863927

<400> 74
aatatatata aatatataaa tatatataaa tatatataca tataaatata taaatatata 60

tatgtaaata tatgtaaata tatgtaaata tatgtatatg tatatatatg taaatgtatg 120

taaatatata taaatatatg taaatatata taaatatacg taaatatata aatatatata 180

actatatata aatatatata aatataaata tataaatata tataaatata tataaatata 240

taaataaata catataaata tataaataaa tacatataaa tatatataaa tatataaaaa 300

tatatataaa tatatatata aatatataaa catatataaa tatataaata tatataaata 360

tataaataca taaaatatat aaatatatat aaatatataa atatatataa atatagataa 420

atatagataa atatataaat atatataaat atataaatat agataaatat ataaatatat 480

aaatataaat atataaaaat atatataaat atataaaaat a 521

<210> 75

<211> 560

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(560)

<223> MAR of chromosome 1 genomic contig; 5712303..5712869

<400> 75
atataattat atatatatta tatattatat ataattatat attatatata atgtataatt 60

atatattata tataatatat ataaatatat atatttttta tataaatata ttatatattt 120

atatattata tataaattta tatatataaa tttttatata ttatatatat ttatatatta 180

tatattgtat atatttatat attacatatt gtatatattt atatattata tattatatat 240

ttatatatta tatattatat atttatatat tatatattat atatatttat atattatata 300

taaattattt atatataata tataaatata tattatataa tataaatttg tatatataat 360

atatatttat attatatata aaatatttat attatatata aaatataata taaatatata 420

catataatat atatattata tatttataat tatatattat atataataca tataatatat 480

aatatataat acatatatat catatatgaa atatatatca tatattatac atattatata 540

taacatatat attatatatc 560

<210> 76

<211> 479

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(479)

<223> MAR of chromosome 1 genomic contig; 8578812..8579290

<400> 76

tatggtatac atatagtata tatggggtac atatatggta tatatatggg ttatatatat 60

gatatatatt atatatgtat atggtatata tatggtatat atattataca tgcatatggt 120

atgtatatgg tatatatatg atatatacat atggtgtata tatatgttat atatgatata 180

tataaggtat atatatggta tatataaggt atatatagta tatatatggt atatataagg 240

tatatattgt atatatatgg tatatataag gtatatatat tgtatatatg gtatatatat 300

ggtttatata tatggtgtgt atatatggtg tttatataca cactttatat actatatatt 360

SEL PCT 012.ST25

atatacacac tatatataat atatattata tatagttaaa tatatggtat atgcaattag 420

atatatggta tatgtaatta tatatatggt atatagatgg tgtatatatg gtatatata 479

<210> 77

<211> 477

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(477)

<223> MAR of chromosome 1 genomic contig; 8579294..8579770

<400> 77

tatagtatat atacacacta taggtaatat actacatatt atatacacac tataaataaa 60

atatataata tataatattt tctatatagt atatattata tattgtatat actatatata 120

atatatacta tagacagtag atactttata tactatagac agtatatact atatactgta 180

tacactatag acagtatata ctatatactg tatacagtat atgtagtgta tatgtagtgt 240

atataatata tagtatatat tatctatact atatacagta tatatagtgt atacataata 300

tatattatat attatatata ctatatacag tatacatagt gtatatgtag tgtataatat 360

atataatgtg tatataaaat atatatacta tatataatat atattatata taatatatac 420

actatatata ctatagatac actatatatt cactatatat actatatata ctatata 477

<210> 78

<211> 331

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(331)

<223> MAR of chromosome 1 genomic contig; 8580024..8580354

<400> 78
actatatgtt atatacataa gatatagtat ataccatata ttatatacat tatatatagt 60

gtatactata tataatgtat ataatatata gtatatatac actatatata ctatgtatat 120

atacactata tatactatgt atatatacac tatatatact atgtatatat acactatata 180

tactatgtat atatacacta tatatactat gtatatatac actatatata ctatgtatat 240

atacactata tatactatgt atatatacac tatatatact atgtatatat agtgtatata 300

tactgtatat gttatagtgt atatatagta t 331

<210> 79

<211> 410

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(410)

<223> MAR of chromosome 1 genomic contig; 8580705..8581114

<400> 79
tatagtctat attatataca gtctatataa tatatagtat atactatata tacttttcct 60

cattctgact atatactata tatatactat atatagtata tgtagtgtat atatacacca 120

tatatactat atatagtata cataccatat atagtatact atacatacca tatatagtat 180

acataccgta tatagtatac tatacttacc atatatagta tacatactat atataatata 240

tctggtgtat atatacacta tatatactat atatactata tatagtatat gtacactatt 300

tatagtattt atagtatata tactgtatat atagtatgta gtatatatac tatatattat 360

gtagactata tataatatag actatgtgta gagtatatat actatatata 410

<210> 80

<211> 433

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(433)

<223> MAR of chromosome 1 genomic contig; 12979167..12979599

<400> 80

atatataata tatatatgtc ctatatataa aatatatcat atatataaat atatatgata 60

tattttatat attaaatata taattatata taaatatata tttatatata aatatattat 120

ttcaatatat ataaatatat ttaaatatat ttaaatagaa tattaaatat ataaatatat 180

aattatattt aatatataaa tatatattaa atatataatt atatttaata tatataaata 240

tatattaaat atataattat atatttatat atttattata tataaatata tatttgttct 300

aaataaatat atattctaaa tatataatat tttatattat ataatatata atataaaata 360

tataataaat atataatata taaataaata aatatttatt ataaaataca tataaatatt 420

aaatatatat taa 433

SEL PCT 012.ST25

<210> 81

<211> 385

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(385)

<223> MAR of chromosome 1 genomic contig; 16336644..16337028

<400> 81
tttatataaa tatctatata aataaatata taaatatata aatataaata tatataaata 60

tataaataaa tatataaata tatataaata taaatatata tataactatg aatttatatt 120

tatataaata tatatctata tgaatataaa tatatattta tataaatata aatatatata 180

taaatatata tatttatata gatataaata tatatataaa tatatatatt tatatagata 240

taaatatata tctatatatg aatatatatc tataggaata taaatatata tctatataaa 300

tataaatata tataagtata aatatatata aatatatatc tatataaata taaatatata 360

tataaatata aatatatata taaat 385

<210> 82

<211> 363

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

SEL PCT 012.ST25

<222> (1)..(363)

<223> MAR of chromosome 1 genomic contig; 20624448..20624810

<400> 82
tatatatata gttatatata tatttatata tatagttata tatatatttt tatatagtta 60

tatatatagt tatatatata gttatatata tatagttata tatatagtta tatatatagt 120

tatatatata tagttatata tatagttata tatatagtta tatatatagt tatatatata 180

tagttatata tatagttata tatatatagt tatatatata gttatatata tatagttata 240

tatatagtta tatatatagt tatatatata gttatatata tagttatata tatatagtta 300

tatatatata gttatatata tatagttata tatatagtta tatatatata gttatatata 360

tag 363

<210> 83

<211> 310

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(310)

<223> MAR of chromosome 1 genomic contig; 566025..566334

<400> 83
tatatataat atatattgta tatattatat attgtatata taatatatat tgtatatatt 60

atatattgta tatataatat atattgtata tattatatat tgtatatata atatatatat 120

tgtatatatt atatattgta tatataatat atatattgta tatattatat attgtatata 180

taatatatat attgtatata ttatatattg tatatataat atatatattg tatatattat 240

atattgtata tataatatat atattgtata tattatatat agtatatatt atatatagta 300

tatataatat 310

<210> 84

<211> 1236

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1236)

<223> MAR of chromosome 1 genomic contig; 1171429..1172664

<400> 84

aaagtattat atgtattata tgtatatgta ttatatatta catatgtatt atatataata 60

tatattatat attattatat attatatatt atatattatt atttatataa tgtattatat 120

attatatagt atatatagta tatataatgt attatatatt atatagtata tatagtatat 180

ataatgtatt atatatagta tatataatgt attatatagt atatatacta tataatgtat 240

tacatattat gtatagtata tgtaatgtat tatatattat atagtatatg taatgtatta 300

tatgtattat atagtatata ttatatatga tgtattattt agtatatata atatatatga 360

tgtattatat aacatatata atatatatga tgtattatat agcatgtata gtatatatga 420

tgtattatat agcatgtata gtatatatga tgtattatat atagcatgta tagtatatat 480

gatgtattat atatagcatg tatagtatat atgatgtatt atatatagca tgtatagtat 540

atatgatgta ttatatatag catgtatagt atatatgatg tattatatat agcatgtata 600

gtatatatga tgtattatat atagcatgta tagtatatat gatgtattat atatagcatg 660

SEL PCT 012.ST25

tatagtatat atgatgtatt atatatagca tgtatagtat atatgatgta ttatatatag 720

catgtatagt atatatgatg tattatatat agcatgtata gtatatatga tgtattatat 780

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attatatata atatatatga tgtattatat atgatgtatt atatataata tatatgatgt 960

attatatata ttattatcta ttatatacga tgtattatat gcaagttatt atgtataata 1020

tataatgtat tatatattat ataatgtata atatataaat atataaatat ataattatgt 1080

ataaatatag aaatatatac attatacatt atatacatta taatgtataa tatataaata 1140

tattatatat aaatgtatac attatatata aatatattat atacattata tataaaatat 1200

gtatatagtt attatacctt atatatacta aacagt 1236

<210> 85

<211> 309

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(309)

<223> MAR of chromosome 1 genomic contig; 1925173..1925481

<400> 85

atatatttat ataaatatat tttatataaa tatatattat ataatattat aatatatgtt 60

atattatata tattttatac aatatataat atatattata tatattttat acaatatata 120

atatatatta tatatatttt atataatata taatatatat tatatatatt ttatacaata 180

tataatatat attatatatt atataatata tattatatat attttatata atatataata 240

SEL PCT 012.ST25

tatattttat acaatatata atgtatatca ttatattata taatgtatat catattatat 300

aatgtatat 309

<210> 86

<211> 312

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(312)

<223> MAR of chromosome 1 genomic contig; 4396756..4397067

<400> 86

cacagtgtat atatagtata tatactgtat atatactgtg tatatacact gtatatacac 60

agtgtatata cagtatatat actatatata cactgtgtat atatagtata tataaattct 120

aggaatatat atactatata tatactatat atataaattc taggaatata tacacactat 180

atatacacta tatatacaca tatatacact atatatatta tacacatata ttatatatat 240

acactatata tacacgagat atataacata tacactatat actatacata acatatatac 300

tatatatact at 312

<210> 87

<211> 398

<212> DNA

<213> Homo sapiens

<220>

SEL PCT 012.ST25

<221> misc_binding

<222> (1)..(398)

<223> MAR of chromosome 1 genomic contig; 56057..56454

<400> 87
atatatatta catattatat atataatata tattatataa tatatattat attatataat 60

atataatata aatataatat aaattatatt atataatata taatataaat ataatataaa 120

ttatataaat ataatatata ttttattata taatataata tatattatat aaatataata 180

tataaattat ataatataat atatattata taatataata tattttatta tataaatata 240

tattatatta tataatatat attttattat ataatatata ttatatattt atagaatata 300

atatatattt tattatataa tatatattat ataatatata ttatatttat atataacata 360

tattattata taaaatatgt ataatatata ttatataa 398

<210> 88

<211> 391

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(391)

<223> MAR of chromosome 1 genomic contig; 56984..57374

<400> 88
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atataattaa actatattat agtatataat atataatata tactatatgt aatattacta 120

SEL PCT 012.ST25

tgatactgat attatattat atataattaa attatattat attaatatat aaattatata 180

taatacataa tatataaatt atattatatt atttatatat aatgtatgcc atataattta 240

tatataatgc attatatata atttatatat aatgcattaa atataaatta tatataatgc 300

attatatata attatatata atgcattata tataatttat atttaatata taaatttata 360

tttaatatat ttatatatta tatataataa a 391

<210> 89

<211> 309

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(309)

<223> MAR of chromosome 1 genomic contig; 469547..469855

<400> 89

atatatatgt aatatatatg ttatatatgt aatatatatg ttatgttata tatgttatat 60

atatgttata tataatatat atgttatata tacgttatat gttatatata tgttatatat 120

aatatatgtt atatatacgt tatatgttat atatgttata tataatatat gttatatata 180

atatatgtta tatatgttat atataatata tgttatatat attatatata atatatgtta 240

tatatattat atataatata taatatatgt gatatataat ataaaatata tgtgatatat 300

attatatat 309

<210> 90

<211> 441

<212> DNA

SEL PCT 012.ST25

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(441)

<223> MAR of chromosome 1 genomic contig; 546190..546630

<400> 90
atacacaaca tatgtgtata tatatagtat atatacacaa catatgtgta tatatatagt 60

atatatacac aatatatgtg tatatatata gtatatatac acaatatatg tgtatatata 120

gtataaatat atactatata tagtatatat agtataaata tatactatat atagtatata 180

catagtataa atatatacta tatatagtat atacatagta taaatatata ctatatatag 240

tatatacata gtataaatat atactatata tagtatatac atagtataaa tatatactat 300

atatagtata tacatagtat aaatatatac tatatatagt atatacatag tataaatata 360

tactatatat agtatataca tagtataaat atatactata tatagtatat acatagtata 420

aatatatact atatatagta t 441

<210> 91

<211> 1367

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1367)

<223> MAR of chromosome 1 genomic contig; 124643..126009

SEL PCT 012.ST25

<400> 91
atatttatat gatatataat atatataata ttatatataa tattatatat gatatataac 60

attatataat attatatatg atatatatta tatatattat atatgatata taatatatat 120

aatattatat atgatattat atatcatata taatatataa aatattatat atgatatata 180

atatatataa tattatatat attatatata ttatatatca tatataatat tctaaatata 240

taatattata tgatatataa gattatatac attatatata atatataata ttatatatga 300

tatataatat tatatacatt atatataata tataatgtat ataatattat atattatata 360

tttatattat atacaatgta tataatatta tatatcatat atatttatat tatatacaat 420

gtatataata ttatatatca tatataatat tatatacaat gtatataata tatattatat 480

atatttatat tatatacaat gtatataata tatattatat atatttatat tatatacaat 540

gtatataata tatattatat atatttatat tatatacaat gtatacaata ttatatatta 600

tatattatat atttatatta tatacaatgt atatattata tattatatat ttatattata 660

tacaatgtat atattatata ttatatattt atattatata caatgtatat attatatatt 720

atatatttat attatataca atgtatatat tatatattat atatttatat tatatacaat 780

gtatatatta tatattatat atttatatta tatataatgt atgtaatatt atatattata 840

tatttatatt atatataatg tatgtaatat tatatattat atatttatat tatatataat 900

gtatgtaata ttatatatta tatatttata ttatatataa tgtatgtaat attatatatt 960

atatatttat attatatata atgtatgtaa tattatatat tatatattta tattatatat 1020

aatgtatgta atattatata ttatatattt atattatata taatgtatgt aatattatat 1080

attatatatt tatattatat ataatgtatg taatattata tattatatat ttatattata 1140

tataatgtat gtaatattat atattatata tttatattat atataatgta tgtaatatta 1200

tatattatat atttatatta tatataatgt atataatatt atatattata tatttatatt 1260

gtatataata ttatatatta tatatttata ttgtatataa tatatattat atatttatat 1320

tgtatataat attatatatt atatatttat attatatata atgtata 1367

SEL PCT 012.ST25

<210> 92

<211> 458

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(458)

<223> MAR of chromosome 1 genomic contig; 58908..59365

<400> 92
tatatgatat atatgatata tatgggatat atatgatata tatgatatat atggtatata 60

tatgatatat agtatatatg atatatatgg tatatatatg atatatagta tatatgatat 120

atatggtata tatgatatat agtatatatg atatatatgg tatatatggt atatatatga 180

tatatgatat atatgatata tatgatatat gatatatatg atatatatga tatatatggt 240

atatatgata tatatggtat atatggtata tatatgatat atatgatata tatggtatat 300

atatgatata tatgatatat atggtatata tatgatatat atgatatata tggtatatat 360

atgatatata tgatatatat ggtatatata tgatatatat gatatatatc atatatatgg 420

tatatatatg atatatatga tatatatcat atatatgg 458

<210> 93

<211> 330

<212> DNA

<213> Homo sapiens

<220>

SEL PCT 012.ST25

<221> misc_binding

<222> (1)..(330)

<223> MAR of chromosome 1 genomic contig; 306867..307196

<400> 93
ataatatata aatatatatg atatatatct atatatatca tatataaata tatatgatat 60

atatctatat atatcatata taaatatata tgatatataa atatatatga tatatatcta 120

tatatatcat atataaatat atatgatata taaatatata tgatatatat ctatatatat 180

catatataaa tatatatgat atatatctat atatcatata taaatatata tgatatatat 240

ctatatatat catatataaa tatatatgat atctatctat atatatcata tataaatata 300

tatgatatct atctatatat atcatatata 330

<210> 94

<211> 353

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(353)

<223> MAR of chromosome 1 genomic contig; 636899..637251

<400> 94
tatgtataca tatacacata tacgtatata tatacatata tacacatata cgtatatata 60

tacgtataca tacatatgta tatgtatacg tatacacaca tatgtatatg tatacgtata 120

cacacatata cgtatatatg tatacgtata cacacatata cgtatatgta tacatatata 180

SEL PCT 012.ST25

tgtgtacata tacgtatata cgtatatgta tacatatata cgtttatgta tatatacgta 240

tatacgtata tatgtatatg tatacatata tacatatatg tgtatatacg tatatacgta 300

tatgtgtata tatacaatat acatacatgc acatatatgt gtatatgcac ata 353

<210> 95

<211> 345

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(345)

<223> MAR of chromosome 1 genomic contig; 1435510..1435854

<400> 95

atcatatata ttatatatca tatatatgat atataaaaat tatatatcat atatatgata 60

tataaaaatt atatatatca tatataatat atataatata ttatatatat aaattatata 120

taatatatat aaattatata tatcatatat atgatatata atttatatat catatatatg 180

atatatataa tatattattt atatataata tattatatat tatataatat gtaatatata 240

ttatatatta catattatat tatttataaa taatatttta taatatatat aatattatat 300

aatatagaat attatatatt atatattaca tattatataa tatat 345

<210> 96

<211> 521

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(521)

<223> MAR of chromosome 1 genomic contig; 39695..40215

<400> 96
tatatatata atagatatta tatatctatt atatatctat tatatatata atagatatta 60

tatatctatt atatatataa tagatattat atatctatta tatatataat agatattata 120

tatctattat atataatata tatctattat atattatata tctattatat ataatatata 180

tctattatat atattatata tctattatat atataataga tattatatat ctattatata 240

taatatatat ctattatata ttatatatct attatatata tgtatctatt atatatatta 300

tgtatctatt atatataata tatatctatt atatatatat tatatataat atatattata 360

tatattatat atctattata tataatatat atctattata tatattatat atctattata 420

tatattatat atctattata tataatatat atctattata tatattatat atctattata 480

tataatatat attatatata tattatatat tgtatatcta t 521

<210> 97

<211> 484

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(484)

<223> MAR of chromosome 1 genomic contig; 1286007..1286490

SEL PCT 012.ST25

<400> 97
atatcatata tattatatat catatatatg atatataaaa attatatatc atatatatga 60

tatatataaa ttatatatat catatataat atatataata tattatatat ataaattata 120

tataatatta tatataaatt atatatcaca tatatgacat ataaattata tatcacatat 180

atgatatata atttatatat cacatatatg atatataatt tatatatcat atatatgata 240

tataatttat atatcatata tatgatatat aatttatata tcatatatat gatatatata 300

atatattatt tatatataat atattatata ttatataata tgtaatatat attatatatt 360

atataatatg taatatatat tatatattac atattatatt atttataaat aatattttat 420

aatatatata atattatata atatagaata ttatatatta tatattacat attatataat 480

atat 484

<210> 98

<211> 244

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(244)

<223> MAR of chromosome 1 genomic contig; 73556..73879

<400> 98
attatatatt atattatata atatataata atattatata attatatatt acattatata 60

atatataata atattatata ataatatata attatataat atataataat attatataat 120

attatataat attatataat atataaatat ataataatat atattatatt atataatagt 180

atatattata ttatataata tatgttatta tattatataa tataaactat tatataatat 240

aata

<210> 99

<211> 463

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(463)

<223> MAR of chromosome 1 genomic contig; 179038..179500

<400> 99
tacaatatat tttctattat atatattttg tattatatat aatatacaat atattttcta 60

ttatatataa tatattttgt attatatata ttacaatata ttttgtatta tataatatat 120

aatacaatat aatatattgt attatataat atataatact atataatata ttgtattata 180

tattatatat aatactatat aatatatttt attatatatt atatataata ctatataata 240

tattttatta tatattatat ataatacaat atataatata ttgtattata atacaatgta 300

ttataatgta ttatatataa tatataatac aatatataat attatatata tttatatata 360

tatatatttt gtattatata ttttgtatta tatatatttt gtattatata tttatatttt 420

atattataat tatgttttgc attatatatt tcatattata tat 463

<210> 100

<211> 390

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(390)

<223> MAR of chromosome 1 genomic contig; 55617..56006

<400> 100
tgtataatat atatacttta tatataatat atatacttta tatatatact atatactaat 60

atatataata tatactatat ataatatata ctaatatata taatatatac actatatata 120

atatatacta atatatatta tatatacttt atataatata tactaatata tataatatat 180

atactttata tataatatat actaatatat ataatgtata tactttatat ataatatata 240

ctaatatata atatatatac tttatatata atatatacta atatatatta tatatacttt 300

atatatataa tatatactta tatattatat atgcttatat ataatatata cactaatata 360

taatatatat actttatata ttatatttta 390

<210> 101

<211> 582

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(582)

<223> MAR of chromosome 2 genomic contig; 1157405..1157986

<400> 101
tgtatatgta tatatacaca tacgcacata tatgtatatg tatatataca catacgcaca 60

SEL PCT 012.ST25

tatatgtata tgtatatata cacatacgca catatatgta tatgtatatg tatatgtata 120

tatacacata tacacatata tgtatatgta tatatacaca tatacacata tatgtatatg 180

tatatataca catatacaca tatatgtata tgtatatata cacatacaca tatatgtata 240

tgtatatgta tatatacaca tacacatata tgtatatgta tatgtatata tacacatata 300

cacatatata catatatgta tacatatatg tgtatatata tacacatata tatacatata 360

tgtatacata tatgtgtata tatacacata tatatacata tatacatata catatatatg 420

tgtatgtata tatacacata tacatatata tgtatatgtg tatatatatt agacagatat 480

atatgtacat atacatatat atgtatatgt atatgtatat gtatatgtat atgtatatgt 540

atatgcatat ataatataca tatacatata tgtatatgta ta 582

<210> 102

<211> 322

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(322)

<223> MAR of chromosome 2 genomic contig; 1858638..1858959

<400> 102

acaccatata tacaccatat atatacatac catatatata ccatatatat acataccata 60

tatataccat atatatacat accatatata caccatatat atacatacca tatatataca 120

ccatatatat acataccata tatataccat atatatacat accatatata taccatatat 180

atacatacca tatatataca ccatatatat acataccata tatatacacc atatatatac 240

ataccatata tataccatat atacaccata tatatacacc atatatacac accatatata 300

SEL PCT 012.ST25

ccatatatat acaccatata ta 322

<210> 103

<211> 914

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(914)

<223> MAR of chromosome 2 genomic contig; 5712196..5713109

<400> 103

aaatatatat tctatatata gaaaatatat attctatata tatagaatat atatagaata 60

tatattctat atatattcta tatatataga atatatatat aaaacatata ttctatatat 120

aaaatatata ttctatatat ataaaatata tattctatat atatagaatg tatataaaat 180

atatattcta tatatataga atgtatataa aatatatatt ctatatatat agaatgtata 240

taaaatatat attctatata tatagaatgt atataaaata tatattctat atatatagaa 300

tatatataac atatatatga aatatatata aaatatatat aaatacatat ttctatatat 360

aaatatatat aaatacatat ttctatatat aaatatatat caatacatat ttctatatat 420

aaatatatat aaatatatat tcatatatat aaaaatatat aaatatatat tcatatatat 480

aaaatatata tgaatatata ttctctatat ataaaatata tataatatat attatatata 540

taaaatatat ataatatata ttatatatat aaaatatata taatatatat tcatatatat 600

aaattatata taaatatata ttcatatata taatatatat aaatatttat ttcatatata 660

aaatatattt aaatatatat ttctatatag aatatatatt ctatatataa aatatatata 720

taaatatatt ttctatatag aaatatatat gaaatatata gaatatatat aaatatatat 780

tatatatact atatatacaa tatatattat atataaaata tatatacaat atatattcta 840

tatattaata tatagaatat atattaacat atatttcaat atattaatat atgaaatata 900

tataaatatt tcat 914

<210> 104

<211> 370

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(370)

<223> MAR of chromosome 2 genomic contig; 5713613..5713982

<400> 104

tatttcatat ataatatata tataaaatat atatttcata tacataatat atataatata 60

aataaaatat atatttcata tatataatat atataatata tataaaacat atatttcata 120

tataatatat ataaactata tatttcatat ataatatata taaactatat atttcatata 180

cataatatat ataatatata tttcatttat attatatata taatatatat ttcatatata 240

taatatataa aatagatata aatatatata aatatatatt tcatatataa tatatataaa 300

atatatatta atatatattt tatatataat atatatattt catatataaa tataaaaaaa 360

tatatatttc 370

<210> 105

<211> 442

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(442)

<223> MAR of chromosome 2 genomic contig; 7481647..7482088

<400> 105
atataaatta tataatatgt tatataatat ataaatatat tatataacat gttatataat 60

atataacatg ttatataata tataacatgt tatataatat ataacatgtt atataatata 120

taacatgtta tataatatat tatgtaatat gttatataat atataatata ttatataaca 180

tgttatataa tatataacat gttatataat atgttatata atatataaat atattatatt 240

atatgttata taatatataa atatattata ttatatgtta tataatatat aaatatatta 300

tattatatgt tatataatat ataaatatat tatattgtat gttatataat atataaatat 360

attatattgt atgttatata atatataaat atattatatt gtatgttata taatatataa 420

atatattata ttatatatgt ta 442

<210> 106

<211> 338

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(338)

<223> MAR of chromosome 2 genomic contig; 9594557..9594894

SEL PCT 012.ST25

<400> 106
tatataaata tataccatat atataaatat atatattcca tatataaata tatatattcc 60

atatatataa atatatatat tccatatata aatatatata ttccatatat ataaatatat 120

atataaatat atatattcca tatatataaa tatatatata aatatatata ttcatatata 180

aatatatata tattccatat ataaaaatat atatatattc catatataaa aatatatata 240

tattccatat atataaatat atatatattc catatatata aatatatata tattccatat 300

atataaatat atatatattc catatatata aatatata 338

<210> 107

<211> 364

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(364)

<223> MAR of chromosome 2 genomic contig; 10519720..10520083

<400> 107
ttatatatat ttataataat atatataagc tatatatatt tatatataat atattatata 60

tattagctat atatatttat ataataatat attatatatt agctatatat atttatatat 120

aataatatat ataagctata tatttatata tattatatat tagctatata tatttatata 180

taatatatta tatattagct atatatttat atataataaa taatatatat attagctata 240

tatatttata tataataata tatataagct atatatttat atataatata ttatatatta 300

gctatatata tttatatata ataatatatt atatattagc tatatatatt tatatataat 360

atat 364

SEL PCT 012.ST25

<210> 108

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(342)

<223> MAR of chromosome 2 genomic contig; 11481943..11482284

<400> 108
tacatataat atataattat atataatata tattatatat tacatatata atatatatat 60

tacatatgta atatatatat tatatatgta atatatatta tatatgtaat atatatatta 120

tatatgtaat atatattata tatatgtaat atatatatta tatatgtaat atatatatta 180

tatgtaatat atatatgtaa tatatatata atatatatgt aatatatata taatatatat 240

gtaatatata tataatatat atgtaatata tatattatat atatgtaata tatatcatat 300

atatgtaata tatatcatat atatgtaata tatatcatat at 342

<210> 109

<211> 415

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(415)

SEL PCT 012.ST25

<223> MAR of chromosome 2 genomic contig; 13499598..13500012

<400> 109
tatatatata tatatatata atataatata atatatatat aaatatatat aatataaatt 60

tatatatata tatttatata tacatatata aatatatatt tatatttata tataaatata 120

tataaatata tataaatata tatttatata tacatatata aatatatatg ttcatataaa 180

tatatatgta tatatacata tataaatata tattatatat gtatatatat aatataatat 240

ataataataa tataatatat attatataaa tataatatat tatatataat atatataata 300

tataatatat aatatataat atataatata tattatatat tatataatat ataaaatata 360

tattatataa tatatataca taatatatat aaataaatat atataaagat ataaa 415

<210> 110

<211> 330

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(330)

<223> MAR of chromosome 2 genomic contig; 16370976..16371305

<400> 110
catttacata tgtatgtata agtatgtata ttacatactt atacatacat acttataaat 60

atataagtat aatacataca tacttataaa tatataagta taatacatac atacttatac 120

atatataagt ataatacata catacttata catatataag tataatacat acatacttat 180

acatatataa gtataataca tacatactta tacatataag tataatacat acatacttat 240

SEL PCT 012.ST25

acatatataa gtataataca tacatactta tacatatata agtataatac atacttatta 300

catatgtata taagtatatt acatacttat 330

<210> 111

<211> 702

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(702)

<223> MAR of chromosome 2 genomic contig; 626641..627342

<400> 111

tatatataca catatacata tataatatat atacatatac atatatatta tatatacata 60

tatattacat atatcatata tacatatata ttatatatac atatatatta tatatatcat 120

atatacatat atatattata tattatatat atcatatata catatatatt atatatatta 180

tatatatcat atatacatat atattatata tattatatat acatatatat tatatatatc 240

atataaacat atatattata tatatcatat atacatatat attatatata ttatatatat 300

catatataca tatatattat atatatcata tataatatat attatatata ttatatataa 360

tatatattat atatacatat atattatata tacatatata ttatatatac atatatatta 420

tatatacata tatattatat atacatatat attatatata tacatatata ttatatatac 480

atatatatta tatatacata tattatatat acatatatat tatatataca tatattatat 540

atatacatat atattatata tacatatatt atatatatac atatatatta tatatacata 600

tattatatat atacatatat attatatata catatattat atatacatat atattatata 660

tacatatata ttttatatat atataatata tattttatat at 702

SEL PCT 012.ST25

<210> 112

<211> 679

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(679)

<223> MAR of chromosome 2 genomic contig; 3196047..3196725

<400> 112
atatattata tattcatata tcataaatat atatattata tattcatata ttatatatct 60

atatatttat atattcatat attatatatc tatatattta tatattcata tattatatat 120

ctatttatat attcatatat tatatatcta tatattttat atattcgtat attatatatc 180

tatatattat atattcgtat attatatatc tatatattat gtattcatat atatctatat 240

attatatata ttcatatata ttataaatta tattcatata gtatatatct attataaatg 300

tatattcata tagtatatat ctatatatta taaatataca tatattatat atttatatat 360

tatatattca tatagatcta tatattatat atattcatat atgaatatat atattatatg 420

tatatatatt ataaatatat ttatatagta tagatattat atagtatatg catatttata 480

ttataaataa tttacatagt atatgtatat ttataaatta tatatattta catattacat 540

gtatatttat atattataaa tacatattta catattataa atatatttat atattatgaa 600

tataatttat atattattac atatttacat atatgcatag ttatatatta taaatatgca 660

tttatgtaaa tatatattt 679

<210> 113

<211> 728

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(728)

<223> MAR of chromosome 2 genomic contig; 3196778..3197505

<400> 113
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ataaatatac atataatatg taaatatata aatatacata tactatgtaa atatatgtta 120

tatatacata tactatataa atatagaata tataaatata catatactat ataaatatgt 180

aatatataaa tatatactat ataaatatac atatactata taaatgtatt tataatatat 240

aaatatacat atactatata aattcatata tgaatatata atatataaat atatataata 300

tatgaatata tactcatata taaatatata tgaatatata tttataatat atagatataa 360

tatgaatata tatttataat atatagatat atattatatg aatatatatt tataatatat 420

agatatatac catatgaata tatattatac actatatgaa tatatattta taatatataa 480

atagatatat actatatgaa tatataatat atatactcta tgaatatata atatatatac 540

tatatgaata tattatatac tgtatgaata tataatatat agatgtatac tatatgaata 600

tataatatat agatatatat actatatgaa tatatataat atatagatat atactatatg 660

aatatatatg atatatagat atatactata tgaatatata atatatagat atatatttat 720

gatatatg 728

<210> 114

<211> 413

<212> DNA

SEL PCT 012.ST25

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(413)

<223> MAR of chromosome 2 genomic contig; 2560638..2561050

<400> 114
atataaatat atatttatat attttatata aatatatata tttatatatt tttatataaa 60

tatatatatt tatatatatt tatataaata tatatattta tatatattta tataaatata 120

taaatatata tatttatata aatatataaa atatataaat atatttatat aaatatataa 180

aatatataaa tatatttata taaatatata aaatatataa atatatttat atataaatat 240

ataaaatata taaatatctt tatatataaa tatataaaat atataaatat ctttatatat 300

aaatatataa aatatataaa tatatttata tataaatata taaaatatat aaatatattt 360

atatacaaat atataaaata tataaatata tttatatata aatatataaa ata 413

<210> 115

<211> 361

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(361)

<223> MAR of chromosome 2 genomic contig; 4965309..4965669

SEL PCT 012.ST25

<400> 115
tatacgtata tatacatata tatacgtata tatatacata tatatacgta tatatacata 60

tgtatatatg tgtgtacatg tatatatata catatgtaca tatatatgta cacatatata 120

tatacatata tatgtacaca tatacatata tatgtacaca tatacatata catatatatg 180

tacacatata tatacatata tatgtacaca catatatata catatatatg tacacacata 240

tatacgtata tatgtacaca catatatacg tatatatatg tacacacata tatacgtata 300

tatatgtaca cacatatata tacgtatata tatgtacaca tatatatata cgtatatata 360

t 361

<210> 116

<211> 325

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(325)

<223> MAR of chromosome 2 genomic contig; 5258150..5258474

<400> 116
tacacacaca tatacatata tacatatata cgtgtatacg tatacgtata tacgtatata 60

tacatatatg tatacgtata cgtatatacg tatatataca tatatgtata cgtatacgta 120

tatacgtata tatacatata tgtatacgta tacgtatata cgtatatata catatatgta 180

tacgtatacg tatatacgta tatatacata catatgtata cgtatacgta tatatgtata 240

tatacgtata tgtatacgta tacatatata cgtatatata cgtatatgta tatgtatata 300

cgtatatgta tatatgtaca tatac 325

SEL PCT 012.ST25

<210> 117

<211> 1508

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1508)

<223> MAR of chromosome 2 genomic contig; 6057499..6059006

<400> 117
atataatata tataaattat ataatatata aaaattaata tataatatat ataaattata 60

taatatataa attaattata taatatatat aaattatata atatataaat taattatata 120

atatatataa attatataat acatataaat taattatata atatataaat tatataatat 180

atacaaatta tatactatat taattatata ttatataatt aattatataa tatatataaa 240

ttatatatta ttaaattaat tatataatat ataaattata taatatataa attaattata 300

taatatataa attatataat atataaatta attatataat atataaatta tataatatat 360

aaattaattg tataatatat aaattaatta tataatatat aatatataat taataaataa 420

ttatatatta attatataat taataaataa ataataaata tatataatta atatataata 480

tacatcatat atatcacata tagattatat aatagttata tattatataa taaattatat 540

ataatatata ataaacatat ataacatatg ttatatatta cataatatag tataatatat 600

aacatatgtt atatattaca taatatagta taatatataa catgttatat attacataat 660

atagtataat atataacata tgttatatat tacataatat agtataatat ataacatatg 720

ttatatatta cataatatag tataatatat aacatatgtt atatattaca taatatagta 780

taatatataa catatgttat atattacata atatagtata atatataaca tatgttatat 840

SEL PCT 012.ST25

attacataat atagtataat atataacata tgttatatat tacataatat agtataatat 900

ataacatatg ttatatatta cataatatag tataatatat aacatatgtt atatattaca 960

taatatagta taatatataa catatgttat atattacata atatagtata atatataaca 1020

tatgttatat attacataat atagtataat atataacata tgttatatat tacataatat 1080

agtataatat ataacatatg ttatatatta cataatatag tataatatat aacatatgtt 1140

atatattaca taatatagta taatatataa catgttatat attacataat atagtataat 1200

atataacata tgctatatat tacataatat agtataatat atatgttata tattacataa 1260

tatagtataa tatataacat atgttatata ttacatatta tagtataata tatatgttat 1320

atattatata atatagtata atatataatg tatgttatat attatataat atagtataat 1380

atataacatg ttatatatta tataatatag tataatatat atgttatata ttatataata 1440

tagtataata tataatatat gttatatatt atataatata gtataatata tatgttatat 1500

attatata 1508

<210> 118

<211> 415

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(415)

<223> MAR of chromosome 2 genomic contig; 7996866..7997280

<400> 118

caattatata atatacatat tatataattg tataaattat acaatcatat aattatatta 60

tatataatat acatataata taattatata taattatata attttataat ataattatat 120

ataattatat aattatatat aatatatatt ataattatat atataatata tatattatat 180

atattatata taatatataa ataatatata taatatatat ataattatat ataataatat 240

atgtaatata tataatatat atataatata ttatttataa ttatatatta tatatatatt 300

ataatatata taattataaa taatatatat tataatatat ataataatat atatataatt 360

atatataata atatatatta taattatata taataatata tataatttat ataat 415

<210> 119

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(526)

<223> MAR of chromosome 2 genomic contig; 8300930..8301455

<400> 119

tatatcatat gatatattat acaatatatc atataatatg atatattata tgatatattg 60

tacaatatat catatgatat atgatatatt atacaatata tcatataagg tatatattat 120

atcatatata atatataata taatatatga tataatatat gatatatgat atataatata 180

tgatatatga tatatgatat ataatatatg atatatgata tatgatatat aatatatgat 240

atatgatata tgatatataa tatatgatat atgatatatg atatgatata tgatatatga 300

tataatatat gatataatat atgatatata ttatatgata tataatatat gatataattt 360

atatgatata taatatatga tatataatat ataatatatg atatgatata tattatatca 420

tatataatat ataatataat atatgatata tattatatat ttttatacat tatatatata 480

aactatataa caatataaca tattatgtgt ataatatata ttacat 526

SEL PCT 012.ST25

<210> 120

<211> 402

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(402)

<223> MAR of chromosome 2 genomic contig; 8576553..8576954

<400> 120
atgtatatta tatacaatat agtatatcat atatagtata tattatatag taatgtatta 60

tatataatgt ataatgtata aatatataat atatactaca tactatacta ttatatatac 120

tatatattat atatgataca tatactatat aatatgctat atattatact atataatatg 180

ctatatatta tactatataa tatgctatat attatactat ataatatgct atatattata 240

ctatataata tgctatatat tatactatat aatatactat ataatatgct atatattata 300

ctatataata tactatatat tatactatat aatatactat ataacatact atatattata 360

tatgatacat atactatatt acatatataa tatatatata ta 402

<210> 121

<211> 477

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

SEL PCT 012.ST25

<222> (1)..(477)

<223> MAR of chromosome 2 genomic contig; 8785649..8786125

<400> 121
tatttatata tatatttata tatatattta tatatattta tatatatatt tatatatata 60

tttatatata tatttatata tttatatata tatattttta tatatttata tatatattta 120

tatatttata tatatttata tttatatata tatttatata tatttatata tatttatata 180

tatatattta tatatattta tatatatata tttatatata tttatatata tttatatata 240

tatttatata tatatttata tatatattca tatatattta tatatatatt catatatatt 300

tatatatata ttcatatata tttatatata tatttatata tatatttata tatatttata 360

tatatttata tatatattta tatatatatt tatatatata tatttatata tatatttata 420

tatatatatt tatatatata tttatatata tatatttata tatatattta tatatat 477

<210> 122

<211> 773

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(773)

<223> MAR of chromosome 2 genomic contig; 10064737..10065509

<400> 122
atattatata tattacatat atattatatt gtatataata tatatattat attgtatata 60

atatatatat tatattgtat ataatatata tattatattg tatataatat atatattata 120

SEL PCT 012.ST25

ttgtatataa tatattatat tgtatatatt atattgtata tattatattg tatacaatat 180

atattatatt gtatacaata tatattatat tgtatataat atattatatt gtatataata 240

tattatattg tatatattat attgtatata atatattata ttgtatataa tatattatat 300

tgtatatatt atattgtata taatatatta tatgtatata atatagtgta tactatatta 360

tataatatat attatataca atatataata tattgtatat catatatgat atattgtata 420

taatatataa tatatgatat attgtatata atatattata tatgatatat tgtatattat 480

atattatata tgatatattg tatattatat attatatatt gtatattgta tattatatat 540

tatatattgt atataatatg ttatatattg tatataatat gttatatatt atatattgta 600

tatatgttat atattatgta ttgtatataa tatgttatat attatatatt gtatataatg 660

tattatatat tatatatatt atatattgta tataatgtat tatatattgt atattatata 720

ttatatattg tatataatat attatataca ttatattata tattatatat tgt 773

<210> 123

<211> 1554

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1554)

<223> MAR of chromosome 2 genomic contig; 1039775..1041328

<400> 123

ataatatatt aaatgtatat ataatatatt aaatataaat atatttataa tatataaata 60

tttatataaa tataaaatat atattaaata taaatatata taaaatatat attaaatata 120

taaaatataa atatatatta aatatatatt aaatatataa aatataaata tatattaaat 180

SEL PCT 012.ST25

atattttaaa tatataaaat ataaatatat attaaatata ttttaaatat attaaatata 240

aatatatatt aaatatattt taaatatatt aaatataaat acatatatta aatatatatt 300

atatatataa aatatataaa atataaatat atattaaata tatataaaat atatatgtta 360

aatatataaa agatatataa aatataaata tatattaaat atatataaaa tatatatata 420

ttaaatatat atattaaata taaatatata taaaatataa atatatgtat taaatatata 480

tattaaatat aaatatatgt attaaatata tattaaatat gaatatatgt attaaatata 540

tattaaatat aaatatatgt attatatata tagaatataa atatatgtat taaatatagt 600

atattaaata taaatatata taaaatatat attaaatatg aatatatata aaatatatat 660

attaaaaata tatataatat aaatatatat aaaatatata tattaaaaat atatataata 720

taaatatata taaaatatat atattaaaaa tatatataaa atatatatat taaaaatata 780

tataaaatat atatattaaa aatatatata aaatatatat attaaaaata tatattaaat 840

ataaatatat atattaaaaa tatatattaa atataactat atattaaata tatattaaat 900

ataactatat attaaatata tattaaatat aactatatat taaatatata ttaaatataa 960

ctatatatta aatatatatt aaatataact atatattaaa tatatattaa atataactat 1020

atattaaata tatattaaat ataactatat attaaatata tattaaatat aactatatat 1080

taaatatata tgaaatataa ctatatatta aatatatatt aaatataact atatgtatta 1140

aatataaata tatgtcttaa atatatatta aatataaata tatgtattaa atatatatta 1200

aatataaata tgtgtattaa atatatatta aatataaata tgtgtattaa atatatatta 1260

aatataaata tgtgtattaa atatatatta aatataaata tgtgtattaa atatctatat 1320

taaatataaa tatatgtatt aaatatatat taaatataaa tatatattaa atatatatat 1380

taaatataaa tatatattaa atataaatat atatattaaa tatatatatt aaatataaat 1440

atatataaaa tatatatatt aaatataaat ataaatataa aatatatatt aaatataaat 1500

acatatatta aatatatgta ttaaatatat atataaaata tatgtattaa atat 1554

<210> 124

<211> 650

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(650)

<223> MAR of chromosome 2 genomic contig; 3944813..3945462

<400> 124
catgatatat tatgtataat atatattata gattacatat aaattatata tataatatat 60

aattatataa tatataatat tatataatat attatatata ttatacaatt atataatata 120

tataatatac aattatataa tatataatat acaattatat aatatataat acaatataat 180

atatatttaa tatattatat aatacatatt taatatatta tatattatat gttatatact 240

aaatatataa tatgtattta atatatacta ttatatatgt aatatattat ataatttatg 300

taacatatta tatattatat atgcaatata ttacatgtta catatatatt acatataata 360

tatgtaatat ataatataca ctatattatt atagtatata atatactata ttatgtaatt 420

atataatata gtatattata cactatatta tattatcata taattatata ttatatacta 480

tattacatat atattatgta atataatatg caatatgtta catatataat atatatgtat 540

tatatagtat atatactata gtatatataa aatatatgct ataatatata ttttatatat 600

tatataatac atataatgta tcatatatta tatataatat attttataat 650

<210> 125

<211> 441

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(441)

<223> MAR of chromosome 2 genomic contig; 5314265..5314705

<400> 125
tataaatata tatgaaatat atataaatta tatataattt atatatacat atataaatta 60

tatataaatt atatataaat tatatataca tatataaatt atatattata tataaaattg 120

tatatattta tatataaatt gtatatataa tttatatata aattgtatat ataatttata 180

tatacaatgt atatattaat ttatatatac attgtatata taatttatat atacattgta 240

tatacaattt atatatacat tgtatataca atttatatat acattgtata tacaatttat 300

atataaatta tattatttat atatagtata tataaatata tatactatat ataaattata 360

tatttattta tatattatat tatttatata taaattatat attatttata tatacattat 420

atataaatta tatattattt a 441

<210> 126

<211> 1169

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1169)

<223> MAR of chromosome 2 genomic contig; 5953971..5955139

<400> 126

SEL PCT 012.ST25

atgtattcat attatatatt tatatataaa taatatacat tcatattata tatttatata 60

taaataatat atattcatat tatatattta tatataaata tataatatat ttatgtataa 120

ataatatata tattcatatt atatatttct atataaataa tatatatatt catattatat 180

atttatatat aaatatataa tatatttata tataaatata taatatattt atatataata 240

tatatattca tattatatat ttatatataa atatataata tatttatata taaataatat 300

atatattcat attatatatt tatatataaa taatatatat tcatattata tatttatata 360

taaataatat atattcatat tatatactta tatataaata atatatattc atattatata 420

cttatatata aataatatat attcatatta tatatttata taaaaataat atatattcat 480

attatatatt tatatataat atatatattc atattatata tttatatatt ctatatattc 540

atattatata tttatatata aataatgtat attcatatta tatatttata tataaataat 600

gtatattcat attatatatt tatatataaa tatatattca tattatatat ttatatataa 660

atatatattc atattatata tttatatata aatatatatt catattatat atttatataa 720

aatatatata ttcatattat atttatatat aaatatatat attcatatat atatttatat 780

ataatatata tattcatatt atatatttat atataatata tatattcata ttatatattt 840

atatataaat aatatatata ttcatattat atatttatat ataaataatg tatattcata 900

ttatatattt atatataaat aatgtatatt catattatat atttatatat aaatatatat 960

attcatatta tatatttgta tataaatata tattcatatt atatatttgt atatatattc 1020

atatatattt atatataaat atataatatt catattatat ataaatatat atattcatat 1080

tatatattta tatatataaa taatatatat tcatattatt tatatatata aataatatat 1140

attcatatta tttatatata taaataata 1169

<210> 127

<211> 653

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(653)

<223> MAR of chromosome 2 genomic contig; 6427669..6428321

<400> 127
tatatatgta tacatatatg tatatatgtg tatatatgta tacatatatg tatatatgtg 60

tatatatgta tacatatatg tatatatgtg tatatatgta tacatatatg tatatatgtg 120

tatatatgta tacatatatg tatatatgtg tatatatgta tacatatatg tatatatgtg 180

tatatatgta tacatatatg tatatatgtg tatatatgta tacatatatg tatacatgtg 240

tacatgtgta tacatatatg tatacatgtg tacatgtgta tacatatatg tatacatgtg 300

tacatgtgta tacatatatg tatatatgtg tatacatata tgtatatatg tgtatatatg 360

tatacatata tgtatataag tgtatatatg tgtatatgta tataagtgta tatatgtgta 420

tatgtatata agtgtatata tgtgtatatg tatataagtg tatatatgtg tatatatgta 480

tacatatatg tatatatgtg tatatatgtg tatatgtata taagtgtata tatgtgtata 540

tatgtataca tatatatgtg tatatatgta tacatatatg tatatatgtg tatatatgta 600

tacatatatg taaatatgtg tatatatgtg tatatgtata taagtgtata tat 653

<210> 128

<211> 414

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(414)

SEL PCT 012.ST25

<223> MAR of chromosome 2 genomic contig; 10890453..10890866

<400> 128
tatattttgt aaatatatat atagtaaata tatgtaaata tatatatttt gtaaatatat 60

atatattttg taaatatatg taaatatata tattttgtaa atatatgtaa atatatatat 120

tttgtaaata tatgtaaata tatatatttt gtaaatatat gtaaatatat atattttgta 180

aatatatgta aatatatata ttttgtaaat ttatgtaaat atatatattt tgtaaatata 240

tgtaaatata tatatatttt gtaaatatat atacatatat attttgtaaa tatataaaca 300

tatatatttt ataaatatat ttataaatat atatattgta aatatattta taaatatatt 360

tataatatat atattgtaaa tatgtttata aatatatata ttgtatatat aaat 414

<210> 129

<211> 496

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(496)

<223> MAR of chromosome 2 genomic contig; 13952568..13953063

<400> 129
taatatacat attatatatt atatattgta tatataatat acatattata tattatatat 60

tgtatatata atatacatat tatatattat atattgtata tataatatac atattatata 120

ttatatattg tatataaat atacatatta tatattatat attgtatata taatatacat 180

attatatatt atatattgta tatataatat acatattata tattatatat tgtatatata 240

SEL PCT 012.ST25

atatacatat tatatattat atattgtata tataatatac atattatata ttatatattg 300

tatatataat atacatatta tatattatat attgtatata taatatacat attatatatt 360

atatattgta tatataatat acatattata tattatatat tgtatatata atatacatat 420

tatatattat atattgtata tataatatac atattatata ttatatattg tatatataat 480

atacatatta tatatt 496

<210> 130

<211> 317

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(317)

<223> MAR of chromosome 2 genomic contig; 16942865..16943181

<400> 130

tctcctagta gttatatata tatatatgtg tatatatata tatcctagta gatatatata 60

tatatatatc ctagtagata tatatatata tatatcctag tagatatata tatatatata 120

tcctagtagt tatatatata tatatatcct aacagttata tatatatata tcctagtagt 180

tatatatata tatatcctag tagttatata tatatatata tcctagtagt tatatatata 240

tatatcctag tagttatata tatatatatc ctagtagtta tatatatata ttatatatta 300

tataatatat atataat 317

<210> 131

<211> 464

<212> DNA

SEL PCT 012.ST25

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(464)

<223> MAR of chromosome 2 genomic contig; 17217049..17217512

<400> 131
acatactata tatatacaca tactatatat actatataca gtatatagta tacatatact 60

atacatatac atatactata catatacata tacatatact aagtatacgt atatacagta 120

catagtatat gtatactata tagtatgtat atatagcata tagtatgcgt atactctata 180

tagcatatag tatgcatata cgctatatag catatagtat gcatatacta tatatagtat 240

agagtatgcg tatactatat atatagtata gagtatgcgt atactatata tatagtatag 300

agtatgcgta tactatatat atagtataga gtatgcgtat actatatata tagtatagag 360

tatgcgtata ctatatatat agtatagagt atgcgtatac tatatatata gtatagagta 420

tgcgtatact atatatatag tatagagtat gtatatatat agta 464

<210> 132

<211> 430

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(430)

<223> MAR of chromosome 2 genomic contig; 19647266..19647695

<400> 132
tgtaaatata tgtaaatata tatttatatt atatattata taaaaatata atatataata 60

tataatatat aaactatata ttaatataat atatataaac tattatataa atacatatta 120

aatatattat atttttaata tttatatatt aaatataata tatatttaat atttatatat 180

taaatatata atatatttaa tatttatata atatatagca tattttatat ttatattata 240

tataacattt tatatttata tttatattta tatatattta atttatattt atattatatt 300

tatatttata ttatatataa cataattata tatattttca tattgtatat aataaagaaa 360

tgtatatttg ttatatataa tatatattat ataatttatt atatattata taatatatat 420

tatataatat 430

<210> 133

<211> 2131

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(2131)

<223> MAR of chromosome 2 genomic contig; 20481223..20483353

<400> 133
tatatataaa tatatttata tttaatatat atttatataa atatattttt atataaatat 60

atatttaata taaatatctt tatatttaat atatatttaa tataaatatc ttatattta 120

atatatattt atatataaat atatatttat atttaatata tattaatatt taatatacgt 180

ttatatttaa tatatatttc tatataaata tatttatatt aacatatatt tatatataaa 240

SEL PCT 012.ST25

tatatttata tttaatatat ttacatataa atatatttat atgtaatata tttacatata 300

aatatattta tatttaatat atatgcatat gtaaatatat ttatatttaa taatatttat 360

atataaatat atttatattt aataatattt atatataaat atatttatat ttaatatata 420

ttaaatatat atttatattt aatatatatt aatatttaat atatatttat atttaatata 480

tattatatat aaacatatat ttatatttaa tatatattat atataaacat atatttatat 540

ttaatatata ttatatataa acatatattt atatttaata tatatttata tttaatatat 600

tatatataaa catatattta tatttaatat atatttatat taaatatata ttatatataa 660

acatatattt atatttaata tatatttata ttaaatatat atttatattt aatatatata 720

tattaaatat atatttatat ttaatatata tttatattaa atatatattt atattaaata 780

tatttatatt taatatatat ttatattaaa tatatattaa atatttaata tatatttata 840

tttaatatat acatatatat ttatatttaa tatatacata tatatttata tttaatatat 900

acatatatat ttatatttaa tatatacata tatatttata tttaatatat aaatttatat 960

tttatatata taaaaatata tatttatatt taatatatat aaatatatat ttatatttaa 1020

tatatatatt tatattgaat atatacataa atatatattt atatttaata tataaacata 1080

tatttatatt tatatattaa atatatattt atatttaata tataaatata tatttatatt 1140

taatatattt atatatacta atatatttat atttaatata tttatatata gatatattta 1200

tatttaatat atttatgtgt attaatatat ttatatttaa tatatttata tattaatata 1260

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tatttatata ttaataaatt tatattttat acagttatat aaatatattt atattttata 1440

cagttatata aatatattta tattttatag ttatataaat atatttatat tttatacagt 1500

tatataaata tatttatatt ttatacagtt atataaatat atttatattt tatacagtta 1560

tataaatata tttatatttt atacagttat ataaatatat ttatatttta tacagttata 1620

taaatatatt tatattttat acagttatat aaatatattt atattttata cagttatata 1680

aatatattta tattttatac agttatataa atatatttat attttataca gttatataaa 1740

SEL PCT 012.ST25

tatatttatg ttttatacat ttatataaat atatttatat tttatacatt tgtatttaat 1800

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atttaatata tatttatata taaatatata ttgatattta atatgtttat atataaatat 1920

atatttatat ttaatatata tgtttatata tcaatatata tttatattta atatatattt 1980

acatataaat atatatttat atttgatata tatttatatt tgatatatat tttatatata 2040

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<210> 134

<211> 842

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(842)

<223> MAR of chromosome 2 genomic contig; 20483478..20484319

<400> 134

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tatatattta tatattaata tatttatgtt taatatatat ttatatatat taatatattt 180

atgtttaata tatatttata tattaatata tttatgttta atatatttat atatattaat 240

atatttatgt ttaatatata tttatatgtt aatatattta ggtatatata tatttatatg 300

ttaatatata tttatattaa tatattatat ttatatataa aagtatatat aatatataaa 360

tattatataa attattatat agtatttttta tatatattta tatataaatt ttatatattt 420

tatatatata aatatatatt tatatataca ttttatatat aaatatatat ttatatatac 480

attatatata taaatatata tatttatatt ttatatataa atatatatat ttatatatac 540

attttatata ttttatatat gtaaatatat atataaattt tatatattgt atatatattt 600

ataaatttta tatatatatt tatatatata atatatataa tatatataaa ttttatatat 660

attatatata tttatatttt atatattata tatttattta tatatattta tatgttatat 720

atatttatat ttatatttat tttttattta tatattttat atatatattt atatatgtat 780

attatatata ttatatatta tataatatat tatatatatt atattatata tttatattat 840

at 842

<210> 135

<211> 645

<212> DNA

<213> Homo sapiens

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<221> misc_binding

<222> (1)..(645)

<223> MAR of chromosome 2 genomic contig; 20897566..20898210

<400> 135

gtatatttat attatatatt atataatata tattatatat taataaatta tatataatat 60

aatatatatg tatatttata tttatgttat aatatacata taattatata tgtatgtata 120

catgtataca tatacgtata tgtgtatatg tatacatata ggtatatgtg tacatgtata 180

catataggta tatgtatatg tatacatgta tacatataat ataattacat atgtatgtat 240

acatacatat gtaattatat tatatatgta tatgtatatt tatataatat ataatatgta 300

ttatatatta tacatgcata tttatatgta tattatatat acacatataa tataattata 360

SEL PCT 012.ST25

tatgtatgta tatatacaca tatatattta tattatatat gtatattata tacatatatt 420

tatattatat atgtatatat atttatcata tttatatgta atatgcatgt gtaataaata 480

atatacacat ttatatatgt atattatata catatattta tattgtatat gtatatatat 540

ttatatatat ttgtatatca tatatttata tattgtatat ttatgtatat tatatattta 600

tatattatat atgtattata taatatatat gtaaatatat attat 645

<210> 136

<211> 722

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(722)

<223> MAR of chromosome 2 genomic contig; 21664541..21665262

<400> 136

tataatatat attatattct atataatatg taaaatatat attatattct atataatgta 60

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ttatatagaa tattataaat aatatattct atattatata tagaatatat tctatatgtt 180

tatattctat atattatata tgaaatagta tataaaatat atataatata tataaaatat 240

gatatataat atatataaaa taatatataa tgtataatat ataaaataat atataatgta 300

taatatataa aataatatat aatgtataat atataaaata atatataatg tatattatat 360

aaaataatat ataatgtata ttatatataa aataatatat aatgtatatt atatataaaa 420

taatatataa tgtatataaa ataatatata atatattata tataaaataa tatataatat 480

attatatata aaataatata tattatatat aaaataatat ataatatatt atatataaaa 540

taatatatat tatatataaa ataatatata atatattata tataaaataa tatatattat 600

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tataatatat tatataaaaa tataaatata ttatataaaa atataaaata taaaatatta 720

ca 722

<210> 137

<211> 305

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(305)

<223> MAR of chromosome 2 genomic contig; 22834991..22835295

<400> 137

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acattatata tttacataat atataataca taatatagaa ttataattat atataataca 180

taatatataa ttatatatat tattatatat gtatttatat tatatataat atattatata 240

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tatat 305

<210> 138

<211> 352

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(352)

<223> MAR of chromosome 2 genomic contig; 25277762..25278113

<400> 138
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atatataata tataatatat tttataatat atataatata ttatatataa tatataatat 120

attttataat atatataata tattatatat attatatatt tatatttatt tatatattca 180

taaatatata tttatatata atatatttta taatatatta tatataatat ataatatatt 240

ttataatata ttataatata taatatataa tatattttat aatatatata atatataata 300

tattatatat ttatatttat ttatatattc ataaatatat atatttatat ta 352

<210> 139

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(342)

<223> MAR of chromosome 2 genomic contig; 25378452..25378793

<400> 139
tatgtacata tatattttat atattatata taatatatat tatatgatat atataatata 60

SEL PCT 012.ST25

ttatataata taatatataa aatatatata atatatatta tattatataa attatattat 120

atatatcata taatatattt tatatattat ataatatata ttatattata tatattttat 180

atattatatt atatattata tatatcatat aatatatatt atattatata ttttatatat 240

tatataatat atattatata tttttatata ttatataata tatattatat attttatata 300

ttatataata catatattat atataatata atatatatta ta 342

<210> 140

<211> 663

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(663)

<223> MAR of chromosome 2 genomic contig; 30209437..30210099

<400> 140

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atatattata tcgtatattg tatattatat attgtatata tgtaatatat gatatgtaca 180

tatgttatat atgtatataa tatactatat tatatattgt atattatata catatataac 240

actattatac aatatataat atagcatatt atatacaata tagcatatac aatatataat 300

atagcatatt atatataata tagtatatta tatacaatat ataatatagc atattatata 360

taatataata tagtatatta tatacaatat ataatatagc atatacaata tagtatacaa 420

tatataatat agcatataca atatagtata ttatatataa tatataatat agcatgtaca 480

atatagtatg ttatatacaa tatataatat agcatataca atatagtata ttatatacaa 540

SEL PCT 012.ST25

tatataatat agcatataca atatattata ttatatacaa tatataatat agcatataca 600

atatagtata ttatatacaa tatataatac agcatataca atatagtata ttacatacag 660

tat 663

<210> 141

<211> 1200

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1200)

<223> MAR of chromosome 2 genomic contig; 31725089..31726288

<400> 141

tgtacttata tattataatg tatatataaa gtatatactt tatatatact tatatattat 60

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ttataatgta tattgtatat attatataca tattatatat gtataatgta tatatacatt 180

atatatgtat aatgtatata tacattatat atgtataatg tatatataca ttatatatgt 240

ataatgtata taatatatac aatatatgta taatatataa tatatacaat atatgtataa 300

tatacaatat atgtataata tacaatatat gtatagtata taatatatat tatatatgta 360

tagtatatta tatattatat atgtatagta tataatatgt ataatgtata tattataata 420

tattatatat aatatctata acaatataat atattgtata tattatatat aatatatatt 480

tatataatat atattatata taatatatta tgtatttatt tatattatat ataatataaa 540

tatatataat ataaataata tttattatat attaatataa atatttatat taatatatat 600

ttattatata taaataatat ctatgatata aataatatat aatatacatg tatatgttat 660

SEL PCT 012.ST25

aatatataca tataatatac atgtgtatat atactataca tgtatatata acatgtatat 720

atatacatgt atatatatta tgtatacatg tatagtatat atacatgtat atatatacat 780

atatactata catgtatata tacatgtata tatatacata tatactatac atgtatatat 840

acatgtatat atacacatat atactataca tgtatatata catgtatata tatacatgta 900

tgttatatac attattataa tatacatata tagtatacat tatatacatt atataatatg 960

cattattata atataatata cattattata atatacatta ttataatata atatacatta 1020

ttataatata cattattata atatacatta taataatata cattattata atatacatta 1080

taatattgaa gtatatatac tataatatat gtatatatta taatgtatat aatatacatt 1140

attatatata agtatgtatt atatataagt atatattata atatatgtat atacatatat 1200

<210> 142

<211> 325

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(325)

<223> MAR of chromosome 2 genomic contig; 32147252..32147576

<400> 142

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ataatttata attatataaa tatataatat atttatatat aatatataat tttattatat 120

attaattata tatataataa atatatataa tatataattt tattatatat taattatata 180

tataataaat atatataata tataataata ttatatacat tatatataaa tataaatatt 240

tatataatat ataatataat atatttattt atatataaat atataatata taattatata 300

SEL PCT 012.ST25

aatatataat atatttatat ataac 325

<210> 143

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(507)

<223> MAR of chromosome 2 genomic contig; 32312662..32313168

<400> 143

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tataaatatt atatttatat tatttatata aatattatat ttatattatt tatataaata 120

ttatatttat attatttata taaatattat atttatatta tttatataaa tattatattt 180

atattattta tataaatatt atatttatat tatttatata aatattatat ttatattatt 240

tatataaata ttatatttat attatttata taaatattta tttatattat ttatataaat 300

attatattta tattatttat ataaatattt atttatatta tttatataaa tatttattta 360

tatttatata aataatatat aaataaatat tttatatgta tataaatatt atttatatta 420

tttatttaaa taaataatat aaattaatat aaatattaat attatttatt ttattataaa 480

taatataaat attatattta tatttat 507

<210> 144

<211> 339

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(339)

<223> MAR of chromosome 2 genomic contig; 33651118..33651456

<400> 144
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ataatatatt atgtatatat aaaatataaa tattatttat atataaaata taaataatat 120

ttatatataa aatataaata ttatattatt tatatataaa atataaataa tatattattt 180

atatataaaa tataaataat atattattta tatataaata atatataaaa tataaatata 240

tattatatat aaataaaata tatatattat atatataaat ttatatataa tatataaaat 300

ataatatata tatttaatat ttattatata atatataat 339

<210> 145

<211> 461

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(461)

<223> MAR of chromosome 2 genomic contig; 45073053..45073513

<400> 145
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SEL PCT 012.ST25

tatacatata tacatgtgta tatatatgta catatacata tatacatgtg tatacataca 120

tatatacatg tacatataca tatatacatg tgtatacata catatataca tgtacatata 180

catatataca tgtgtatact tacatatata catgtacata tacatatata catgtgtata 240

tatacatata tacacgtaca tatacatata tacatgtaca tatatacatg tatacatata 300

tacatgtaca tatgtacata tatacatgta tacatatata catgtacata tgtacatata 360

tacatgtata catatataca tgtacatatg tacatatata catgtataca tatatacata 420

tgtacatacg cacagataga catatataca tatgtacata c 461

<210> 146

<211> 1162

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1162)

<223> MAR of chromosome 2 genomic contig; 45487691..45488852

<400> 146

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tctattatat atattatatt atattatatt atatataata tctattatat atattatatt 240

atctatataa tatctattat atattatata ttatattata tataatatct attatatata 300

ttatattata ttatatataa tatctattat atctattata tatattatat atatctatta 360

tatctattat atatattata tataatatct attatatcta ttatatatat tatatataat 420

SEL PCT 012.ST25

atctattata tctattatat tatattatat ataatatcta ttatatctat tatatatatt 480

atatatatct attatatcta ttatatatat tatatataat atctattata tctattatat 540

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tattatatat tatatatata atatctatta tatctattat atctattata tatatatcta 660

ttatatctat tatatatatt atatacataa tatctattat atctattata tatattatat 720

atataatatc tattatatct attatatata tactatctat tatatctatt atatatatta 780

tatatgtact atctattata tctattatat ctattatata tatactatct attatatcta 840

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ctattatata tctattatat atattatttt atattatata tagtatctat tacatatatt 960

atattatatt atatataata tctattatat atattatatt atattataaa taatatatat 1020

aatatctgtt atatataata gatattatat ataatatata atatatataa tagatattat 1080

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<210> 147

<211> 562

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(562)

<223> MAR of chromosome 2 genomic contig; 45516233..45516794

<400> 147

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SEL PCT 012.ST25

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atatacatat tatatatatt atatatacat attatatatt atatataata tatacatatt 180

atatattata tataaatatt atatattata tataaatatt atatatataa atattatata 240

ttatatataa atattatata tcttatatat aaatataata tataatatat ataatattta 300

tatattatat ataaatatta tatatattat ataatattat atataatata taaatatata 360

tattatataa atattgtata tattatataa atattatata tattatatat aaatattata 420

tatattatat aaatatatat aaatatataa aatatataaa tatgtaaaat ttatatttat 480

aaatatataa tataaatata taaatataaa tataaattat atataatata taatatatta 540

tacataatat atactatata ta 562

<210> 148

<211> 801

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(801)

<223> MAR of chromosome 2 genomic contig; 45727251..45728051

<400> 148

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atatagaata tatatataga atatatatat atagaatata tatatagaat atatatatat 180

agaatatata tatatagaat atatatatat agaatatata tatatagaat atatatatag 240

aatatatata tagaatatat atatatagaa tatatatata gaatatatat atatagaata 300

SEL PCT 012.ST25

tatatataga atatatatat atagaatata tatatagaat atatatatat agaatatata 360

tatagaatat atatatatag aatatatata tagaatatat atatatagaa tatatatata 420

gaatatatat atatagaata tatatataga atatatatat atagaatata tatatagaat 480

atatatatat agaatatata tatagaatat atatatatag aatatatata tagaatatat 540

atatatagaa tatatatata gaatatatat atatagaata tatatataga atatatatat 600

atagaatata tatatagaat atatatatat agtatatata gaatatatat atatagtata 660

tatagaatat atatatatag aatatatata tagaatatat atatatagaa tatatatata 720

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atatatatat atatatagaa t 801

<210> 149

<211> 346

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(346)

<223> MAR of chromosome 2 genomic contig; 50937238..50937583

<400> 149

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attctattat aatatatatt atatataata tatattctat tataatatat attatatata 180

atatattcta ttatgatata tattatatat aataacatat attatatata atatatattc 240

tattatataa aatatatatt atataaaata tatattctat tatataaaat atatattata 300

SEL PCT 012.ST25

taaaatatat attatattat ataaaatata tattatacta tatata 346

<210> 150

<211> 462

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(462)

<223> MAR of chromosome 2 genomic contig; 55672627..55673088

<400> 150

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tatttataat atatatcata taaataatat atatttataa tagatatcat ataaataata 180

tatatttata atagatatca tataaataat atatatttat aatagatatc atataaataa 240

tatatattta taatagatat catataaata atatatattt ataatatata tcatataaat 300

aatatatatt tataatatat atcatataaa taatatatat ttataatata tatcatataa 360

ataatatata tttataatag atatcatata aataatatat atttataata gatatcatat 420

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<210> 151

<211> 401

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(401)

<223> MAR of chromosome 2 genomic contig; 56081352..56081752

<400> 151
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tatacatata tacatgtata tgtgttatat acatatacat atatacatgt atatgtgtta 180

tatacatgtg tatgtgtata tgtatatata catatatgtg tatgtgcatg tgtatatata 240

catatatgta tatgtgtata tgtatatata catatatgta tatgtgtatg tgtatacgta 300

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<210> 152

<211> 765

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(765)

<223> MAR of chromosome 2 genomic contig; 56404208..56404972

<400> 152
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aaagaatata tattatatat tatgtaaaga atatatatta tatataatat ataaagaata 120

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ataatatata aagaatatat aatatataat atataaagaa tatatattat atataatata 240

taaagaatat atattatata taatatataa agaatatata ttatatatta tataaagaat 300

acatatatat aatatataaa gaatatatat tatatataat atataaagaa tatatattat 360

atataatata taaagaatat atattatata taatatataa agaatatata ttatatataa 420

tatataaaga atatatatta tatataatat ataaagaata tatattatat atattatata 480

aagaatatta tatattatat aaagaatata tattatatat aatatataaa gaataaacat 540

atatactata tataaagaat atacattata tatactatat ataaagaata tacattatat 600

atactatata taaagaatat atataatata taaagaatat acattatata taatatataa 660

agaatatatt atatattata taaagaatac attataatat aaagaataca ttatatataa 720

tataaagaat acattataat atataaagaa tatatataat atata 765

<210> 153

<211> 443

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(443)

<223> MAR of chromosome 2 genomic contig; 61953416..61953858

<400> 153

tttatatatt atagataaaa ttatattata ttacatgtaa tatataatat gtaaaatata 60

ttatattaca tatataatat ataatatgta aaatatatta tattacatat ataatatata 120

SEL PCT 012.ST25

atatgtaaaa tatattatat tacatatata atataaaata ttacatataa tatattttac 180

ataaatatat attatctatt acatatttat tatatgtaat aatatgtaca tatgtataaa 240

tatgtatata tttatacata tgtatatatt atatatacat atatatgtat atattatata 300

tacatatata tgtatatatt atattatata tacatatata tgtatatatt atattatata 360

tacatatata tgtatatatt atattatata tacatatata tgtatatata ttataaatat 420

gtataataaa gatttatatg taa 443

<210> 154

<211> 372

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(372)

<223> MAR of chromosome 2 genomic contig; 62076211..62076582

<400> 154

tatatataat tatatatgta attatatatc agtatatata attatatata attatcaata 60

tatataatta tatataatta tcaatatata taattatcaa tagatatata taattatata 120

tataattata tataattata tatcagtata tatacttata taattatata tatgtatata 180

taattatatg tataaattat ctataagtat atataactat aatatatatc aattatatat 240

acttatgtat aattatatat actgatatat aattatacat aattatatat atcaattata 300

tataattatg tataattata tatacatata tataattata tatataaatt atatgtaatt 360

atataattac ac 372

<210> 155

SEL PCT 012.ST25

<211> 484

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(484)

<223> MAR of chromosome 2 genomic contig; 62158581..62159064

<400> 155
attatatata atataaaaat tatacatatt attttattat atattatata cataatatat 60

atatttcata tataatatat attatatata atataaaata tatattatgt ataattatat 120

ataaaatata ttatataatt atatataaca taaaatatat ataatatata attatatata 180

atataaaata tatatataat ataaaatata tattatatgt aattatatat aatataaaat 240

atatatataa tataaaatat atattatata taattataat ataaaatata tattatatag 300

tatatattat ataaaatata tattatatat aattatatat tatataaaat atatattata 360

tataattata taatataaaa tatatattgt atataattat atataatata aaatatatat 420

aatatatgaa ataagatata tactatatat aatatatata atttacatat aagatatata 480

tcat 484

<210> 156

<211> 644

<212> DNA

<213> Homo sapiens

<220>

SEL PCT 012.ST25

<221> misc_binding

<222> (1)..(644)

<223> MAR of chromosome 2 genomic contig; 68145036..68145679

<400> 156
tatatatatg ctaatatatg taatatatat tatatatatg ctaatatata tatgctaata 60

tataatatat attatatata aatatataat atatatttat ataaatatat aatatattat 120

atataaatat ataatataaa tatatataat atatactata ttatatatta tgtataacat 180

ataatacata tttgttatat ataatatata tattatatgt tatatattat atattatata 240

taatataaca atatatttta tatattatat gttatatatt atatattata tataatataa 300

cataatatat aatatatatt atattatata ttacatatat tagcaatatt atatataaaa 360

tatatataat atatataaaa tatatataaa aatataaaat atatatcaaa atataaacta 420

tataatatat aaaaatatat tatatataat atataaaaat ataaactata taatatataa 480

aaatatatta tatataatat ataaaaatat attatatatt atatataaaa atatattata 540

tataatatat aaaaatatat ataaaatata aaaaatatat ataaaatata aaaaatatat 600

aaaataatat aaaatatata atatataata atataatata taat 644

<210> 157

<211> 530

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(530)

<223> MAR of chromosome 2 genomic contig; 71257289..71257818

<400> 157
atatctatta tatttatata ctttatataa attatatcta ttatatttat atactttata 60

taaattatat ctattatatt tatatacttt atataaatta tatctattat atttatatac 120

tttatataaa ttatatctat tatatttata tactttatat aaattatatc tattatattt 180

atatacttta tataaatata taattatatt tatatacttt atataaatat aattataaat 240

atatttatat actttatata aatataatta taaatatatt tatatacttt atataaatat 300

aattataaat atatttatat actttatata aatataatta taaatatatt tatatacttt 360

ataattatat gttatattta taattatatt tatataattc ataattatat acattatgtt 420

tatagttata taatttataa ttatatacat tatatttata tttatataat ttataattat 480

ataaattata taaattatat aaattatctt taatttatat tatataatct 530

<210> 158

<211> 337

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(337)

<223> MAR of chromosome 2 genomic contig; 73413615..73413951

<400> 158
acttatatta tatataacta tattattgta tattaatata aattaatgat atataatata 60

ttaattatat attattatat gtgatataaa atacttatat ttatactgta tatatgtata 120

tacacacata tatgtatata tgtatatata cacatatgta tatatgtata tgtatatatg 180

SEL PCT 012.ST25

tatactgtat atatgtatat acacacatat atgtatatat gtatatgtat atatgtatac 240

tgtatatatg tatatacata tatacatata tgatatatat cacatatatg tgatatataa 300

atatatttat ataaatataa tattaatatt tatatta 337

<210> 159

<211> 1340

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1340)

<223> MAR of chromosome 2 genomic contig; 77011049..77012388

<400> 159

atgtatttta tatagtatat attatgtatt atattgatat aattatataa caattattta 60

tatataaaat aacaaataaa tatataaaat aataaatata tatttattat taaataataa 120

atatatattt attattaaat aataaatata taaagtaata aatatatatt tatatattaa 180

ataattcata tatatttata tattaaataa ttcatatata tttaaataat taatacatat 240

ttaaataatt aatatatatt tatataatat atatttatat attaaataat taatatatat 300

ttatagatta aattaatata tatttatata ttaaattaaa tttaatatat tatatattta 360

tataatttaa atttaataat ttatataatt taatttaatt taatataatt aaaatatatt 420

aaacattata taatatataa tatatttaat atataatata tatttaatat ataatatatt 480

taatatataa tatatttaat atataatata tatttaatat ataatatatt taatatataa 540

tatatttaat atataatata tatttaatat ataatatatt taatatataa tatatattta 600

atatataata tatttaatat ataatatata tttaatatat aatatattta atatataata 660

tatatttaat gtataatata tttaatatat aatatatatt taatgtataa tatatttaat 720

atataatata tatttgatgt ataatatatt taatatatat ttgatgtata atatatttaa 780

tatataatat atatttgatg tataatatat ttaatatata atatatattt gatgtataat 840

atatttaata tataatatat atttgatgta taatatattt aatatataat atatatttga 900

tgtataatat atttaatata taatatatat ttgatgtata atatatttaa tatataatat 960

atatttgatg tataatatat ttaatatata atatatattt gatgtataat atatttaata 1020

tataatatat atttgatata taatatattt aatatataat atatatttga tatatattta 1080

atatataata tatatttgat atataatata tttaatatat aatatatatt tgatatataa 1140

tatatttaat atataatata tatttgatat ataatatatt taatatataa tatatatttg 1200

atatataata tatttaatat ataatatata tttgatatat aatatattta atatataata 1260

tatatttgat atataatata ttttcttatt aattatttat atataatata taaatatata 1320

ttaattaatt atatattaaa 1340

<210> 160

<211> 937

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(937)

<223> MAR of chromosome 2 genomic contig; 78226855..78227791

<400> 160

tgtgtatata tacatatatg tgtatctatg tgtatatata catatgtgta tatatacata 60

tatgtgtata tatacatatg tgtatatatg tgtatatatg tgtatatata catatatgtg 120

tatatatgtg tatatatgtg tatatataca tatatgtgta tatatgtgta tatatacata 180

tgtgtatata tgtgtatata tacatatatg tgtatatatg tgtatatata catatatgtg 240

tatatatgtg tatatataca tatatgtgta tatatgtgta tatatgtgta tatatacata 300

tatgtgtata tatgtgtata tatacatata tgtgtatata tgtgtatata tacatatatg 360

tgtatatatg tgtatatgtg tgtatatata catatatgtg tatatacaca catatatgtg 420

tatatatgtg tatatataca tatatgtata tatacatata tgtgtatata tgtgtatata 480

tacatatatg tgtatatatg tgtatatata catatatgtg tatacataca tatatgtgta 540

tatatgtgta tatatacata tatgtgtata catacatata tgtgtatata tgtgtataca 600

tacatatatg tgtatacata catatatgtg tgtatatgtg tatacataca tatatgtgtg 660

tatatatgtg tatacatatg tgtgtatatg tgtatatata catatatgtg tgtatatatg 720

tgtatatata catatatgtg tgtatatatg tgtatatata catatatgtg tgtatatatg 780

tgtatatata catatatgtg tgtatatatg tgtatatata catatatgtg tgtatatatg 840

tgtatatata catatatgtg tgtatatatg tgtatatata catatatgtg tgtatatatg 900

tgtatatata catatatgtg tgtatatatg tgtatat 937

<210> 161

<211> 1350

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1350)

<223> MAR of chromosome 2 genomic contig; 79287748..79289097

<400> 161

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tatatatatt atatatatag taactgttct attatatata tattatatat atttctgttc 60

tattatatat tatatatatt atattatata ttatatgtaa tatattatat atattataag 120

taatatatta tatatattat atgtaatata ttatatatat tatatgtaat atattatata 180

tattatatgc aatatgttat atatattata tgcaatatgt tatatatatt atatgcaata 240

tattatatat attatatgca atatattata tataatatat gtaatatatt atattatata 300

ttatatgtaa tatcttatat attatatgta atatattata tatattatat gtaatatctt 360

atatatatta tatgtaatat attatatatt atatgtaata tattatctta tatatattat 420

atgtaatata ttatattata tattatatgt aatatatatt atatgtaata tattacatat 480

tatatgtaat atatattata tgtaatatat tacatattat atgtaatata tattatatgt 540

aatatattac atattatatg taatatatta catattatat gtaatatatt atatgtatta 600

tatgtaatat attatatgta ttatatgtaa tatattatat gtattatatg tattatatgt 660

aatatattat atgtattata tgtaatatat tatatattat atgtaattat attatatgta 720

atatattata ttatatatta tatatattat atgtaatata ttatattata tattatatat 780

attatatgta atatattata ttatatatta tatatattat atgtaatata ttatattata 840

tattatatat attatatgta atatattata ttatatatta tatatattat atgtaatata 900

ttatattata tattatatat attatatgta atatattata ttatatatta tatatattat 960

atgtaatata ttatattata tattatatat attatatgta atatattata ttatatatta 1020

tatatattat atgtaatata ttatattata tattatatat attatatgta atatattata 1080

ttatatatta tatatattat atgtaatata ttatattata tattatatat attatatgta 1140

atatattata ttatatatta tatatattat atgtaatata ttttatatta tatatattat 1200

attatatatt atatgtaata tattatatta tttattatat attatatatt atatgtaata 1260

tattatatta tttattatat atattatatt atttattata tataatatat tatattatat 1320

atattatatt atatatattt ctgttctaat 1350

<210> 162

<211> 332

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_difference

<222> (1)..(332)

<223> MAR of chromosome 2 genomic contig; 81142998..81143329

<400> 162
ctatgtatat aactatatat aactattata taacttaata agatatataa ctattatata 60

acttaataag ttatatataa ctattatata taacttaata agttatatat aactattata 120

taacttaata agttatatat aactattata taacttatta agttatatat aactatatat 180

aacttaataa gttatatata actattatat aacttaataa gttatatata actattatat 240

aacttaataa gttatatata actattatat aacttaataa gttatatata actatatata 300

acttatatac aacttattaa gctatatata ta 332

<210> 163

<211> 327

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(327)

<223> MAR of chromosome 2 genomic contig; 84019536..84019862

SEL PCT 012.ST25

<400> 163
actgacagta tacatactgt atatatatac agtatgtata catatacagt atgtatacta 60

tatacagtat gtatactgta tatatatata cagtatgtat actgtatata tatacagtat 120

gtatacgtat gtatactgta tatatgtatt atagtgtata tatgtattat agtgtatata 180

tgtattatat atattatagt gtatgtatta tatgtgtata tacatataat atattataca 240

tatacatatg cacaatatgt atatgtatta tatgtattca tatacatata tgtatatgta 300

taatatatgt atacatataa tacacat 327

<210> 164

<211> 407

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(407)

<223> MAR of chromosome 2 genomic contig; 1448030..1448436

<400> 164
tatataatat atattacata tatattatat ctatattatt tatattacat atgtaatata 60

tattatattt atattattta tataatatat tatatatatt atattattta tatgtaatat 120

atttatattg tttatatata ttatatttat attatttata tataatacat attatattta 180

tattatttat atataatata tataataaat atataatata tataaaaata tatatattta 240

atatatctat aatatatatt atatatatta tatataatat atataattgt acatatattt 300

attatatata ttatatatat aatatatatt ataaatataa tatataaata tatttataaa 360

tatatataaa tattatattt atacattata tttatataca tattata 407

SEL PCT 012.ST25

<210> 165

<211> 1959

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1959)

<223> MAR of chromosome 2 genomic contig; 2117630..2119588

<400> 165
tatacatgtt atagtgtata tagtatacta atatataatg tatgtatgtg tatacatata 60

cacatataat atacacatat ataatatata tagtatataa taatgtataa tatataatat 120

ataatataaa atgtatagta tactacatat ttatatatag tatatagtat gcatagtaca 180

tatatactat atatgtagta tactatagtg tatatatagt acaccatata tagtataaat 240

atactatata gtatatgtac tatatatata ctatatagta tatacagtat acatatatag 300

tatacctata ctatatagta tatatagtgt gcgtatacta tatagtatat atagtgtgcg 360

tatactatat agtatatata gtgtgcgtat actatatagt atatatagtg tgcgtatact 420

atatagtata tatagtgtgc gtatactata tagtatatat agtatacata tatagtgtgc 480

gtatactata tagtatatat agtatacata tatagtatgc gtatactata tatagtatac 540

atatatagta tatctagagt atatgtagta tgtatagtat atatagtcta catactgtat 600

atacagtata tatatactct atagtatact atacagtata gtatactata tagtatacaa 660

tatatgtata ctatagaaac acactatata tagtatacta tatatactat atactatata 720

ctatatatag tatactatat atactacata ctatatatag tgtatgtata gtatatataa 780

actatatata gtgtatatag tatatatatt atatataata tatattatat tatattatac 840

SEL PCT 012.ST25

tatatattat atgtatatta tagtatatta tactattata tattatatat tatattatat 900

attatataat ataatataat tatatattat aaaatatata ttttatatt atatattttt 960

aaatatttta taatatatat tttataatat atatattata attattttat atataatata 1020

aaatataata aatattttat aatatatatt tttaaaatat aatatttata tattataaaa 1080

atataaatat ataatatatt atatattata tatagtataa tatataatat gttatatagt 1140

atcttatact attatactat atatattata tagtgtatat atagtatact atatatagtg 1200

tatatagtgt atactatagt gtatatagtg tatactatag tgtatatagt gtatactata 1260

tacactgtat atagtagtgt atactatata cactgtatat agtagtgtat actatataca 1320

ctgtatatag tagtgtatac tatatacact gtatatagta gtgtatacta tatacactgt 1380

atatagtagt gtatactata tacactgtat atagtagtgt atactatata cactgtatat 1440

agtagtgtat actatataca ctgtatatag tagtgtatac tatatacact gtatatagta 1500

gtgtatacta tatacactgt atatatagta tattatatat actatatatg tatatatagt 1560

atacatatat attatatata cagtatatat agtatatata ctatgtagta tatatagtat 1620

atatactata tagtatgtat agtatactat atagtatata tagtatatta tatagtatat 1680

atactatata gtatatatag tatattgtat atatagtata tatactatat agtatatata 1740

gtatattgta tatatagtat attgtatata tagtatacat agtatgtata tatagtatat 1800

atagtataca tatatagtat gtacacagta tatatagtct atatgtatac tacatatagt 1860

atacatgtat actatactac atatagtata catgtatact atactacata tagtatacat 1920

gtatagtata ctacatatac tatacatgta tagaatact 1959

<210> 166

<211> 520

<212> DNA

<213> Homo sapiens

<220>

SEL PCT 012.ST25

<221> misc_binding

<222> (1)..(520)

<223> MAR of chromosome 2 genomic contig; 2119984..2120503

<400> 166
tatgtatgca tcgtatacat atatagtata tatatgtatg catcgtatac atatatacag 60

tatatatagt atgcatcgta tacatacagt atactatata tacagtatat acagtatact 120

atatatacag tatatacagt atactatata tacagtatat acagtatact gtatatacag 180

tatatacagt atatatagta tactatatat acagtatata tactatgtat tctatatata 240

gtatagtgta catagtatac atatagtata cactatacta tatatagtat actatatata 300

ctctatatag tatatatagt atactatata tagtatatat gtatactata tatagtgtat 360

atatatacta tatatagtgt atatatatac tatatatagt atatatatac actatatatt 420

gtatagtata gtgtatatat agtatagtat atgtatatat acacatgtat acatgtatat 480

atgtatacta atatatacta atatatgtat aaatatatat 520

<210> 167

<211> 954

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(954)

<223> MAR of chromosome 2 genomic contig; 2578285..2579238

<400> 167

tattatatat aactttataa tatataatat atattatata taactttata atatataata 60

tatattatat ataactttat aatatataat atatattata tataacttta taatatataa 120

tatatattat atataacttt ataatatata atatatatta tatataactt tataatatat 180

aatatatatt atatataact ttataatata taatatatat tatatataac tttataatat 240

ataatatata ttatatataa ctttataata tataatatat attatatata actttataat 300

atataatata tattatatat aactttataa tatataatat atattatata taactttata 360

atatataata tatattatat actatatata atatataact ttataatata taatatatat 420

tatatactat atataacttt ataatatata atatatatta tatattatat ataactttat 480

aatatataat atatattata tataacttta taatatataa tgtatattat atattatata 540

ttatatatta tatataactt tataatatat aatgtatatt atatattata tataacttta 600

taatatataa tatataatat aatatataac tttataatat atatatcata tattatatat 660

aactttataa tatatatcat atattatata taactataat atatatatca tatattatat 720

ataactataa tatatatatc atatattata tataacttta taatatatat atcatatatt 780

atatataact ttataatata tatcatatat tatatataac tttataatat atatcatata 840

ttatatataa ctttataata tatattatat ataactttat aatatatatc atatattata 900

tataacttta taatatatat catatattat atataacttt ataatatata tcat 954

<210> 168

<211> 452

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(452)

<223> MAR of chromosome 2 genomic contig; 3836217..3836668

<400> 168
tttatatata aatatatatc ttatatatat ttatatataa tacatatata tcttatatat 60

ataaaatata tatacatatt tatatataaa atacatatgt attatataca tttatatata 120

atacatatgt attatataca attatataat acatatgtat tatatacaat tatataatac 180

atatttataa atatatatat ttatatttat atatatttat atataaataa atatatattt 240

atagatttat ttatataaat atatatttat ataaatatat atttatatat atttatataa 300

atatatattt atatatattt ctatatatat atataaatat atgtataaat atatatattt 360

atacatatat tcatataaat atatatattt atacatgtat ttatatgaat atatatttat 420

acatgtaatt atatgaatat atatttatac at 452

<210> 169

<211> 417

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(417)

<223> MAR of chromosome 2 genomic contig; 3837666..3838082

<400> 169
gatatatata tttatataaa tatatatata aagagatata tttatatatt tatttatata 60

aatatatttc tttatataaa gatatatgta aatatattta tttatataaa tatatttata 120

tatgtaaata tatatttata tatttatata tttatatatt tatttatata aatatatata 180

tttatatatt tatttatata tataaaaata tataaatata aatatatata aatatatata 240

attataaata tagaaataaa tataaatata aatatataaa tatatataaa tataaatata 300

tataaatata aatatatata aatataaata tataaatgta taaatatata aatataaata 360

tatataaata tgtataaata tataaatata taaatatata aaaatatata taaatac 417

<210> 170

<211> 1197

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1197)

<223> MAR of chromosome 2 genomic contig; 6294846..6296042

<400> 170

tatatactaa tatgtatata taaatatata aatatatata cacgtgtata tataaatata 60

tatgtatata taaatatata tacatatatg tatataaaaa tatatacgta tatacgtata 120

tacgtatata tagatatata cgtatatacg tatatacgta tatatagata tatacgtata 180

tacgtatata tagatatata cgtatatacg tatatacgta tacatgtgta tatacgtata 240

tacacatata cgtatacatg tgtatatacg tatatgtata cattatatat acgtatatat 300

acatatatgt atacatgtat atataaatat atacatatat gtatatatta tacatatatg 360

tatatataat atatatatta tatataatat atatattata tataatatat atattatata 420

taatatatat attatatata atatattata tattatatat aatatataca tatataatat 480

attatatatg tacatatgta cataatgtat atatgtatat atataatata tatgcacatg 540

tatatataat atatgtatat tatatataca tatgtatata tgtacatatt atatatgtat 600

atatgtacct attatatata catatgtata tatgtaccta ttatatatac atatgtatat 660

SEL PCT 012.ST25

atgtacatat tatatataca tatgtatata tgtacatatt atatatacat atgtatatat 720

gtgcatgcat atataatata taatatatta tagattataa tattatatac atatcatata 780

ttatatactt atatatacat gtatatatta tatacatatt atatattata tacatataat 840

atatgtatat aatatataca tatattatat attatatata atacattatg ttatatatta 900

tgttatataa tatatattat ataatataca tatattatat ataatatata catatataat 960

aaataatata taattatata tataatatat gcatataaat atgtaatata ttttatatta 1020

tatatgatca tatataatat gacatattat atatgattat atatatgata tattatatat 1080

gattatatat attatatata aatatatgat tatatataat catatatata aatatatgat 1140

tatatgatta tatataaata tatatatatg attatatgat tatatataat tgattat 1197

<210> 171

<211> 362

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(362)

<223> MAR of chromosome 2 genomic contig; 6506971..6507332

<400> 171

tatatatagt gtatactata tatacgctat atgcacacat aaactatata tacagtatat 60

aatatgcgta tactatatac acagtatata ctacatgtat actatatata gtatataaga 120

tatatactat gtatataata tatatactag gtatatatat ccatatatat actatatact 180

atagtatata catatatatg tacgtatata tgtatatgta catatatatg tagtatgtat 240

atatatacat atatacacac tatagtatat acatatatat actatatata ccctatatag 300

SEL PCT 012.ST25

agtatattat atacagtata ctatatatac tatatatacc ctatatagag catgtctatg 360

ct 362

<210> 172

<211> 2578

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(2578)

<223> MAR of chromosome 2 genomic contig; 6507395..6509972

<400> 172

ggtatactat atatactata gagtatactt tatagtatat atacctatat tatatatata 60

tacatacact gtatagtata tatggtatat atactatata tggcatatat agtttatata 120

tatactatat atggtatata tagtttatat atatactata tatggtatat atagtttata 180

tataccatat atggtatata tagtttatat agtacatata gtatatatac acactgtata 240

gtatatatta tgtagtatat atactatata tactgtatat atagtataaa tactatatat 300

agtatacact atatactata cactatatat actatatact atatactata tatagtatac 360

tatatagtat atagtatact ctatatgtac tatagagtat actatatata ctatacataa 420

aatatttttta tatatagtac agcgtatact atatactata tatagtatac tctatatgta 480

ctatagagtg tagtatatac tatacagtat actctatata tactatacag tacactatat 540

atactatata tagtatattt tatatatagt acagtatata cagtatatat attatactat 600

atgtagtaca tatatagttt agtatatata gtatatatac tatactatat gtactacata 660

tataatagta tatatagtat atatactata ctatatgtag tacatatata gtttagtata 720

SEL PCT 012.ST25

tatactagta tatagatata tagttatata gatatataat agtatatata gtatatatag 780

catatatagt atatatgcta tatatactat atagcatata ctatatacta tatatacagt 840

atatatagca tatatagcat atataatata tatacttttg atatacatac tatatacagt 900

atatatagta tatatactgt ataaatatac tatatatacc gtatatgcac actatatgct 960

atatatacta tatacactat atacagtata tatagtacac tatactatat aaagtatata 1020

tagtatacag tacactatac tatatacatt atatatagta tatattatac atagtatata 1080

gtatataaat agtatatata gtatatacag tatatatata gcatacttta tatagtatac 1140

acagtatata gatactatat atgctatata tagtatctat atactgtata ttatatatac 1200

taatatagta tatatgtata tatatactgt atatataata tatacatata tagtatatat 1260

actatacata cacactatac atatgtatat atactataca tactatatac tatatatcct 1320

atatatacta tatagtatat tatatatcct atatatacta tatagtatat tatatatcct 1380

atatatacta tatagtatat tatatatact atataccata tatactatat atactgtata 1440

gtatactata tatactatat agtatactgt atatactata tagtatactg tatatactat 1500

atagtatact gtatatacta tatagtatac tgtatatact atatagtata ctgtatatac 1560

tatatagtat actgtatata ctatatatac tatatagtat actgtatata ctatatagta 1620

tactatatat actatatacc atatatacta tgtatatact atatatagta tatactatgt 1680

atatgctata tatagtatat atagtatata tgctatatat agtatatata gtatatatgc 1740

tatatataca gtctatatat agtatatata ctatatagac tatatatata gcatatatac 1800

tatatatact atatataata tatatggtat atacatagta tctatatgta gtatctatat 1860

atagtaccta tatatactat atataggtac tatatatagt atatatactt tatatagata 1920

ctatatatag tatatatact ttatatagta tatatagtat atgtagcata tatagtatat 1980

atagtatata tagtatatag tatgtatagt atatatagat tatattgtat atacagtata 2040

tatactgtat atactatata aatagtacat acagtatata cagtatatat gtactatata 2100

tagtatatac agtatataca gtatatatgt accatatata gtatatacag tatatacagt 2160

atatatgcac tatatgttat atacagtata tacagtatat atgtactata taaatagaat 2220

SEL PCT 012.ST25

atactctata tacagtatat atgtactata taaatatata cactatgtac agtatatatg 2280

tactatataa atagtatata cactatatac agtatatatg tactatatag tgtatacagt 2340

atatacagta tataggtact atatatggta tatacagtat atatgcacta tatggtatat 2400

acagtatata tgcactatat atggtatata cagtatatat gtactatata tggtatatac 2460

agtatatatg tactatatat ggtatataca gtatatatgt actatatatg gtatatacag 2520

tttatacagt atatatgcac tatatatggt atatacagta tacatgtact atatatgg 2578

<210> 173

<211> 598

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(598)

<223> MAR of chromosome 2 genomic contig; 7770400..7770997

<400> 173

gtgtattgta tatacatata cgtatctacg tatatacata tatgtattgt atatacatat 60

atgtattgta tatacatata tgtatatacg tatatacata tatgtattgt atatacatat 120

atgtatatac gtatatacat atatgtatat acgtatatag atatacatat atatgtattg 180

tatatacata tatgtatata catatataca tatatattga tatacatata tatgtattgt 240

atatacatat acaatatatg tatatataca tatacatata caatatatgt atatacatat 300

atatgtattg tatatacata tatatgtatt gtatatacat atattgatat acatatatgt 360

atatatacat atatgcatat atgtatatat acatatatgc atatatgtat atatacatat 420

atacatatgt acatatatac atatatacat atatgtatat atacatatat acatatgtac 480

SEL PCT 012.ST25

atatatacat atatacatat gtacatatat acatatatac atatgtacat atatacatat 540

atagatatat atacacatat atagatatac ttatatgtat atatacatac atacatat 598

<210> 174

<211> 1048

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1048)

<223> MAR of chromosome 2 genomic contig; 8332422..8333469

<400> 174

cattatatat aatatataat atattattat atataatata tataacatta tatatagtat 60

atatgacata tataacatat attatatata acatatataa aatataacat attatatata 120

acatatataa aatataacat atattatata taacatatat aaaatataac atatattata 180

tataacatgt ataaaatata acatatatta tatataacat gtataaaata taacatatat 240

tatataacat gtataaacta taacatatat tatatataaa atatattata tgttatatat 300

tataaataaa atatattata tgttatatat tataacatat tatataaata atatataata 360

tataacatat attatataaa taatatataa catatattat ataaataata tataacataa 420

catatattat ataacatata acatataaca tatattatat ataacatata acatataaca 480

tatattatat ataacatata acatataaca tatattatat ataacatata acatatatta 540

tattatatat aacatataac atatattata ttatatataa catataacat atattatatt 600

atatataaca tataacatat attatattat atataacata taacatatat tatattatat 660

ataatatata acatatatat tatatataat atataacata taacatatat tatatataat 720

SEL PCT 012.ST25

ataatatata acatatatta tatataatat aatatataac atatattata tataatataa 780

tatataacat atattatata taatataata tataacatat attatatata atataatata 840

taacatatat tatatataat ataatatata acatatatta tatataatat aatatataac 900

atatattata tataatataa tatataacat atataatata taacatatag catatataat 960

atataacata taacatatat tatatataac atataacata tattatatat aacatataac 1020

atatataata tgtaacatta tatataac 1048

<210> 175

<211> 375

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(375)

<223> MAR of chromosome 2 genomic contig; 8909678..8910052

<400> 175

tatatacaca tatatacgta tgaatatata tacacatata cgtatgaata tatataccca 60

tatacgtatg aatatacaca tatatatacg tacgtatata tatacacata tatacgtacg 120

tatatatata cacatatata cgtacgtata tatatacaca tatatacgta cgaatatata 180

tacacatata tacgtacgaa tatatataca catatatacg tacgaatata tatacacata 240

tatacgtacg aatatatata cacatatata cgtacgaata tatatacaca tatatacgta 300

cgaatatata tacacatata tacgtacgaa tatatataca catatatacg tacgaatata 360

tatacacata tatac 375

<210> 176

SEL PCT 012.ST25

<211> 563

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(563)

<223> MAR of chromosome 2 genomic contig; 10572503..10573065

<400> 176
atttataata tatatgtata aatatatgta tatatttata tttaaatata tgtatatata 60

tttatattta aatatacgta tatatattta tatttaaata tacgtgtata tatttatatt 120

taaatatacg tgtatatatt tatatttaaa tatacgtgta tatatttata tttaaatata 180

cgtgtatata tttatattta aatatacgtg tatatattta tatttaaata tacgtgtata 240

tatttatatt taaatatacg tgtatatatt tatatttaaa tatacgtgta tatttatatt 300

taaatatacg tgtatattta tatttaaata tatgtatgta tttataaata tatatttaaa 360

gtatatattt ataaatgtat acatgtatat ataaatatat atattttaaa tatatattta 420

tatatatatt tatatattta tataagtata tatatattta aatatatgta tatatttata 480

tatttatata agtatatata tttaaatata tgtatatatt tataatatat attttaaata 540

tatatttata tatttattat ata 563

<210> 177

<211> 595

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(595)

<223> MAR of chromosome 2 genomic contig; 11609694..11610288

<400> 177
tataaatact atatatagta tatataatat tatatatact atatataaat atatgtagta 60

taaataatat ataatataga tatataatat aatataatat gttataaata taaatatatt 120

tatataattt aatttataat atataatata taatatataa tttaatttta taatatataa 180

tatataattt aattttataa tatataatat ataatatgta aattatatat aatttaatat 240

atctaaatta tataatttaa atataaatat aatataaata tatctaacat aatatacata 300

acataaatat atatagtata tatagtacat ataaatatat atagtacata tagtatatat 360

aaatatatag tatatataaa tatagtatat ataaatatat agtatatata tagtatatat 420

aaatatatag tatatataaa tatatatagt atatataaat aatatatagt atataaataa 480

tatatattat taaatataat aataatttat tatatatact atatattatt atgtattata 540

ttatatatat tattttatat ttaatatata ttatttttata tattatattt aatat 595

<210> 178

<211> 662

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(662)

<223> MAR of chromosome 2 genomic contig; 12699804..12700465

<400> 178
gtatatatat atatatatat atggtgtata tatatatata tatatatggt gtatatatat 60

atatatatat atggtgtata tatatatata tggtgtatat atatatatgc tgtatatata 120

tatggtatat atatatggta tatatatatt tgctatatat atagcagatc tgctatatat 180

atatatttgc tatatatata gcagatctgc tatatatatt tgctatatat atgctatata 240

tatgctacat atatgctata tatatgctat atatatgcta tatatatgct atatatatgc 300

tatatatatg ctacatatat gctatatata tgctacatat atgctatata tatgctatat 360

atatatgcta tatatatgct atatatatat gctatatata tgctatatat atatgctata 420

tatatgctat atatatatgc tatatatatg ctatatatat gctatatata tagcatatat 480

atatagctat atatatgcta tatatatagc ttatatatat gctatatatg ctatatatat 540

gctatatata tagctatata tatgctatat atagctatat atatgctaca tatatgctat 600

atatatgcca tatgtatgct atatatatgc tatatatata tgctatatat atgctatata 660

ta 662

<210> 179

<211> 649

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(649)

<223> MAR of chromosome 2 genomic contig; 12821904..12822552

<400> 179

SEL PCT 012.ST25

tatgtaatat tatatatata aattatatat tatacatatg taatattata tatatataaa 60

ttatatatta tacatatgta atattatata tatataaatt atatattata catatgtaat 120

attatatata tataaattat atattataca tatgtaatat tatatatata taaattatat 180

attatacata tgtattatat atataaatta tatattatac atatataata tatatataaa 240

ttatatatta tacatgtata atatatataa attatatatt atacatatat aatatatata 300

aattatatat tatacatata taatatatat aaattatata ttatacatat ataatatata 360

taaattatat attatacata tataatatat ataaattata tattatacat atataatata 420

tataaattat atattataca tatataatat atataaatta tatattatac atatataata 480

tatataaatt atatattata catatataat atatataaat tatatattat acatatataa 540

tatatataaa ttatatatta tacatatata atatatataa attatatatt atacatatat 600

aatatatata aattatatat tatacatata taatatatat aaattatat 649

<210> 180

<211> 3191

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(3191)

<223> MAR of chromosome 2 genomic contig; 15356889..15360079

<400> 180

tacaattata tataactata aatataatat aatatatatt atctatatta catattaata 60

tataatatat attacctatt aatatataat ataatatata taatatatat tacctattaa 120

tatataatat aatatatata atatatatta cctattaata tataataaaa tatatataat 180

atatattaca tattattata taatatatat tataaacat atataacata tactatatat 240

tatataacat atataattgt atatgtatta tatatattat atatacttat acataatata 300

taaataatta aatatatgtt ataaatataa caaatatata acatatataa catatataac 360

atatatataa ttacataaaa tatataatac ataatatata ttatgcaaca tattatataa 420

tatataacat ataatgtata ttatattata tcatatataa tacataatat ataatatatg 480

atataatata atatattata tatgatataa tataatatat tatatatgtt ataatataat 540

atatattata tataggatat attataacat attacatatg atataataaa ttttatctta 600

tatataggat atattataat atatcacata tagcatatat taaaatatat tacatatagt 660

atattatata tactatatgt atatatacat atagtatatt atagtatatt atacagtata 720

tattatatat actatatata gtagtataca gtatatatta tatatactat atatagtagt 780

atacagtata tattatacag tatatattat atacactata ttatatatta tgtataatat 840

atactatata tagtatatta tgtagtatat attaaacata atagatatat agtatatact 900

atagataata gatattatat agtatatagt atatattata tataatatat ataatatata 960

ttatatacat atatgatata tgatatatta tatataatat atataatata taatatatgt 1020

aatataatac atattatata taatatatgt aatataatat aatatataat atatgtaata 1080

taataatata tattatataa tataacatat ataaatataa taatatatat tatatgatat 1140

aacatacata aatataataa catatataat atatattata tattatattg tatatatgat 1200

atactatata ttacacatta tacattattt ataatatata attaatatat aacatatatt 1260

agataacata taattatatc tgtaacatat ataagatata attacatata taacatatat 1320

aattatatat atatttatct aattatatat gaaattatat atgacatata aaattatata 1380

ttatatatgt tatatgtatt atatattata tatgttatat atgttatata taacatatat 1440

aacatatata acacacacat ataacatata taacatatat tacatatata acatatataa 1500

cacatatata attatctaac atagataata tatataatat ataatataac atatatatta 1560

tatattatac actctattat attatatata ttatacataa tatataatat atatgatata 1620

atataataca ttgtatatac gatataatat atattgtaca tagtataata tacatatata 1680

SEL PCT 012.ST25

gtatattatg tataacataa tatatagtat attatgtata acataatata tagtatatta 1740

tgtataacat aatatatagt atattatgta taacataata tatagtatat tatgtataac 1800

ataatatata gtatattatg tataacataa tatatagtat attatgtata acataatata 1860

tagtatatta tgtataacat aatatatagt atattatgta taacataata tatagtatat 1920

tatgtataac ataatatata gtatattatg tataacataa tatatagtat attatgtata 1980

tataatatac atattatata gtatattatg tatataaat atacatatta tatagtatat 2040

tatgtatata taatatacat attatatagt atattatgta tatataatat acatattata 2100

tagtatatta tgtatatata atatacatat tatatagtat attatgtata tataatatac 2160

atattatata gtatattatg tatatataat atacatatta tatagtatat tatgtatata 2220

taatatacat attatatagt atattatgta tatataatat acatattata tagtatatta 2280

tgtatatata atatacatat tatatagtat attatgtata tataatatac atattatata 2340

gtatattatg tatatataat atacatgtta tgtagtatat tatgtatata taatatacat 2400

gttatgtagt atattatgta tatataatat acatgttatg tagtatatta tgtatatata 2460

atatatataa ggtgtatata tattatgtat atataatata taaggtatat atattatgta 2520

tatataatat atataaggtg tttatataat gtatatataa tatataaggt atgtatatta 2580

tgtatatata atatgtatat tatatataat atatattatt tatatacatt atgtatctat 2640

ataatatata ttatgtatat attaggtatc tatataatat atattatgta tatatattat 2700

gtatctatat aatatatata ttatgtatat atattatgta tctatataat atatatatta 2760

tatgtatatt atgtatctat ataatatata taatgtatat agatatatta tatattatgt 2820

atatatatta tgtatctatt ttatatataa tgtatataga tatacaatat atattatgta 2880

tatattatgt atctatataa tatatattat ttatatagat atatatatta tgtatatata 2940

cataatatat tacatattat gtatatatac ataatatata atatattatg tatatataca 3000

taatatataa tatattatat attacatata ttatatataa tatattatat tatgtatata 3060

tattatgtat atataatgta tatataatat ataaagtgta tatatattgt gtatatataa 3120

tgtatatata ttacatatat tatgtgtata tatattatac ataatatata tactacatta 3180

SEL PCT 012.ST25

tacataatat g 3191

<210> 181

<211> 314

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(314)

<223> MAR of chromosome 2 genomic contig; 728676..728989

<400> 181
tgtgtatata tgtatatata atatatatta tataatatgc atatgtataa aatatgtata 60

ttatatatgt atattttata tatatgtata tattatatgt atattttata tatgtatatt 120

ttatatatat gtatatatta tatatgtata ttttatatat atgtatatat tatatgtata 180

ttttatatat atgtatatat tatatatgta tattttatat atatgtatat attatatatg 240

tatattttat atatatgtat attttatata tatgtatatc atatatatgt atatattata 300

tatatgtata tctt 314

<210> 182

<211> 423

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

SEL PCT 012.ST25

<222> (1)..(423)

<223> MAR of chromosome 2 genomic contig; 737493..737915

<400> 182
ataatatata gtgtctttta tattatctaa tatgtaatat aatgtatttt atattatgta 60

ttttatatta tataatatat aatataatgt attttatatt atatgttata taatatatag 120

tgcattatat attatgttat attatatata ttttatttat ataaattata tattatatgt 180

tattttatat atattatata acatataata taacaatgca ttatatatta taaaatatat 240

aatacattac atatattata taatatataa tacattacat atattatata atatataata 300

cattatcata tattacaaat attacattag tataatagta attataatat aatatattat 360

atattacata tattatatta atgtaatagt aattataata taatatatat tatattttat 420

att 423

<210> 183

<211> 724

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(724)

<223> MAR of chromosome 2 genomic contig; 1069556..1070279

<400> 183
tattataata tattatatac attatattgt atatatacta tatatggtat atatagtata 60

cataatataa aatgtatatt gtaatataca ttatatatat acatagtgta cattatataa 120

SEL PCT 012.ST25

tataaataaa tgtatattat aatatacatt ataatataat agtgtactat gtatatagta 180

tatataatgt atattataat gtattatata gtataatata atataatata cattatatag 240

tattgcatta tatatgctat ataatatata atatattatg tatatataca ttatatatac 300

tatattatat agtacatata atgtatatta tatagtatat ataatataat acattataca 360

tacaatatat aatgtatatt atatagtatg tataatgtaa tacattatac atagtacata 420

aagtatatta taatatatta taatatataa tatacattat atattataat gtatataata 480

tattgtatat atactatata taatgtatat acaattatat ataattgtat atatacatgt 540

atatgtatat gtatatatac atgtatatgt atgtgtatat atacatatat gtatatgtat 600

gtgtatatat gtatatgtat atatgtatat gtatacgtat atatgtatat acaatgtata 660

tataatgtat ataaaaatat ataatatata caatatgtat ataatgtata taattatata 720

atat 724

<210> 184

<211> 383

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(383)

<223> MAR of chromosome 2 genomic contig; 2719918..2720300

<400> 184

atatttatat tttatatatt atttatatat aaatatatat ttatatttta tatattattt 60

atatataaat atatatttat attttatata ttatttatat ataaatatat atttatattt 120

tatatattat ttatatataa atatatattt atattttata tattatttat atataaatat 180

atatttatat tttatatatt atttatatat aaatatatat ttatatttta tatattattt 240

atatataaat atatatttat attttatata ttatatattt atatattata tatatttata 300

ttaatttgtg tataatatat attattaaat ataataaata tatttatttt tatatattat 360

ataaaaatat ataatatata aaa 383

<210> 185

<211> 309

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(309)

<223> MAR of chromosome 2 genomic contig; 4994249..4994557

<400> 185
tataatatat aattgttata acattataac aattatatat tatatataat acaattatat 60

aatatatatt atataattgt aatatataat ataattatat aatatatatt atataatata 120

atatataata tatcatatat gttatatatt ttattatata atatatatta tatataatat 180

tatatataat atatattata tataatatta tatataatat atattatata taatatattt 240

atatatatta tatataatat atattatata ttaaatatta tatatataat atatataaca 300

ttattgtta 309

<210> 186

<211> 740

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(740)

<223> MAR of chromosome 2 genomic contig; 5034916..5035655

<400> 186
tttatatata aaatattata tataatatta tatataatat tttctatata aaatgtgtat 60

ataattatat ataattatat aaaatataat atagaatatc taataatgta taatatataa 120

catataaaaa taatattatt taatatataa tattttatat ataatatttt tatatataat 180

ataatatata ttttatatat aattattaat tatataatta atatataata tatattttat 240

acataattat taattatata taattaatat ataatatatc ttatacataa ttatcaatta 300

tatataatta atatataata tatattttat acataattat taattatata taattaatat 360

ataatatatc ttatacataa tatatataaa tatattatat ataatatata ttatatataa 420

tattatatat aatatatatt atatatataa aatttatata taatattata tataatatta 480

tatattttat atacaatatg atatataata taatttatat attatatata tttatatata 540

attattatat aaattatata aatataaatt atatatttat atataattat tatataaatc 600

attatataat tattataatt ataatatata atatataata atattatata taatatatag 660

tattctatat aaataatata acatatattt tatatagaat attatatata atataatata 720

tattttatat agaatattat 740

<210> 187

<211> 847

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(847)

<223> MAR of chromosome 2 genomic contig; 6074678..6075524

<400> 187
aatatagaca taaatatata tgcataaata tatatatgca taaatatata taaaaatata 60

tataaatata tacataaata tatataaata tatacaaaaa tatatataaa tatataaaaa 120

aatatataaa tatatataca catatataaa tatatataca tacatatata aacatatata 180

cataaatata tatgtataaa tatatataca cataaatata tgtatgaata tatatacata 240

aatatatatg tataaatata tatacataaa tatataaaga tatatacata aatatatata 300

aatatatata cataaatata tataaatata tataaataga tatataaata tatatataaa 360

tatataaata tatatataaa tatataaata tataaaaata gatatataaa tatatatata 420

aatatataaa tatatatata aatatatata aatatataaa tatatatata aatatatata 480

aatatataaa tatatataaa tatataaata tatatataaa tatatataaa tatataaata 540

tatataaata tatataaata tataaatata tatataaata tatataaata tataaatata 600

tatataaata tataaatata taaatatata tataaatata taaatatata taaatatata 660

taaatatata aatatatata aatatatata aatatataaa tatatataaa tatatataaa 720

tatatataaa tatataaata tatataaata tatataaata tatataaata tatataaata 780

tataaatata tatataaata taaatatata taaatatata aatatatata taaatatata 840

taaatat 847

<210> 188

<211> 784

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(784)

<223> MAR of chromosome 2 genomic contig; 6108986..6109769

<400> 188
atttatttat atatttaata tataaaatat atatttaata tataaaatgt atatatatac 60

atatattata tataatacaa tatatattat atataatata tattatatat aatattatat 120

attatattat aatataatat atattatata taatataata tatattatat attattatat 180

ataatataat atatattata tattattata tataatataa tatatattat atattattat 240

atataatata atatatatta tatattatta tatataatat aatatatatt atatatatat 300

tttatatata taatatataa tatatatatt atatatatat tttatatata taatatataa 360

tatatatatt atatatatat tttatatata taatatataa tatatatatt atatatatat 420

tttatatgta taatatataa tatatatatt atatatatat tatatatata taatatgtaa 480

tatatatatt atatatatat tatatatata atatatatta tacataaaat atatattata 540

tataatatat ataatatata ttatatataa aatatatttt atgtataata tatattatat 600

ataatatata atgtatattt atatataaaa tatatattta tatacaatgt atatttatat 660

ataaaatata tatttatata caatgtatat ttatataaat atgtgtttaa tatatgaaat 720

atatatttat atataatata tatttaatct ataaaatata tattaaatat atatttatat 780

ttaa 784

<210> 189

<211> 381

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(381)

<223> MAR of chromosome 2 genomic contig; 10389032..10389412

<400> 189
tatacacata tagagtatat agagtatata tagagtatat ctatagagta tatatgtata 60

tagagtatat aatacagcct accatatata tagtatacat atatatatac tctatatact 120

atatatatag tgtgtatata tatagtatag accctaccat atatatatat aggagtatat 180

atatatacac actcctacta tatatagtat gtatatagag agtatataga gtatatatac 240

agtatatata cacagtatat atatgccata tatagtatct atatacttat atatagtatg 300

tatctatata cttatatata gtatgtatct atatactata tatagtatgt atctatatac 360

tatatagagt atatatgtat a 381

<210> 190

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> misc_difference

<222> (1)..(507)

<223> MAR of chromosome 2 genomic contig; 11097807..11098313

<400> 190

SEL PCT 012.ST25

aattatatat aatttattat atataatttt atatttataa tatttttata tacatatttt 60

atatatcttt ataattatat attacatata taatattata taatatatat aatatatata 120

atatatatta tatattatat aatatatatt atatatatta tatataatat atataatata 180

tataatatat ataatatata taatatataa tatatattat ataatatata ttatatataa 240

tatatattat atataatata tattatatat aatatataat atatataata tatataacat 300

ataataatat attatacata atttatatat aatttttata taattatata tatttatata 360

tttttatata attatatata tttatatatt tttatataat tatatatatt tatatatttt 420

tatataatta tatatataat ttttatataa atatatataa ttttatataa ttttatataa 480

ttataaaata tataattata tataatt 507

<210> 191

<211> 329

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(329)

<223> MAR of chromosome 2 genomic contig; 11234628..11234956

<400> 191

ttatagttaa atatataaat ataaaatata cagtttata cagtatatat aaaatataca 60

atatataata cataatacat tagttatata tactatatat actatatata ctacacgtat 120

agtatatata tgaaactata tatatactat acgtgtagta tatatatgaa actatatata 180

tactatacgt gtagtatata tatgaaacta tatactatac gtatagtata tatatgaaac 240

tatatatact atatatactt aactataatt gtatatagtt aaaaatataa atataaaata 300

tacagttaaa tatattaata tataatagt 329

<210> 192

<211> 584

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(584)

<223> MAR of chromosome 2 genomic contig; 797844..798427

<400> 192
tattatttta tgttataaat agataaaaat atatactaat atatatgtac ttatatatac 60

atcaatatat aatgtattat tttatactaa cgtatattat atatactagt atataatcta 120

tattatttta tatgttataa atatataata aaatatataa atattttatg catatattaa 180

tatataatat atactaacat gctaatttat atatacttat atataattta tatagtatat 240

aatatataaa tgtatataat acataattta tatatttata tattaatagt ttatatatta 300

gtatatatac taattttata tactaataaa taaattatat aatatataaa ttatatatta 360

tagtacataa tatatattat atagttaaat aactatgtaa ctataatata taactatata 420

tgatatacag ttatatataa tataaatttt acatacagta tataaattat atactataca 480

tttatataca tatggtatat aaattatata ctatacattt atatacatat ggtatataaa 540

ttgtatacta tataatgtgt attagtatat atactaatat atac 584

<210> 193

<211> 363

<212> DNA

SEL PCT 012.ST25

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(363)

<223> MAR of chromosome 2 genomic contig; 1093824..1094186

<400> 193
tatacacaca catatatata cacatatata tacacatata tatatacaca tatatataca 60

catatatata cacgtatata tgtatacaca tatatatgta tatatataca catatataca 120

cacatatata cgtgtatata cgtatatacg tacatatata cgtgtatata cgtatatgcg 180

tacatatata cgtgtatata cgtatatgcg tacatatata cgtgtatata cgtatatgcg 240

tacatatata cgtgtatata cgtatatgcg tacatatata cgtgtatata cgtatatgcg 300

tacatatata cgtgtatata cgtatatgcg tacatatata cgtgtatata cgtatatgcg 360

tac 363

<210> 194

<211> 545

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(545)

<223> MAR of chromosome 2 genomic contig; 3456187..3456731

SEL PCT 012_ST25

<400> 194
tattataata tatatttata tattataata tatattatat tatatattta tatattataa 60

tatatattat attatatatt tatatattat aatatatatt atattataat atatatttat 120

attataatat attatattat aatatatatt atattattat atattataat ataatatata 180

ttataatata tattatatta taatttatat attatatata ttataatata tattatatta 240

tatatatatt tatattataa tatatattat tatatattat atattataat ttatattata 300

ttacaatata tattataaat atatatatta tattataaat atatattttt atattacaat 360

atatattata aatatatatt ttatattaca atatatatta taaatatata tattatatta 420

caatatatat tataaatata tattatatta caatatatat tatattataa tatatattta 480

tatatgatat attatattta atatattata taacataata tataatatat aatatattaa 540

tataa 545

<210> 195

<211> 356

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(356)

<223> MAR of chromosome 2 genomic contig; 5001567..5001922

<400> 195
tataaaatat atgttatata tataatatat attatataat atataatata tataatatat 60

aaaatatata aaatatataa tatataatat aatatataat atatataata tataaaatat 120

atataatata aaatatatat aatatataat atatataata tataatacat ataatatata 180

SEL PCT 012.ST25

atatataata tataatatat ataatatata atatataata tataatatat ataatatata 240

atatataata tatataatat ataatatata atatataata tataaatata taaatatata 300

tacacacata cacacacata tatgcatata tatacatata catgtgtaca tagata 356

<210> 196

<211> 321

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(321)

<223> MAR of chromosome 2 genomic contig; 5457330..5457650

<400> 196

tatacaatat attataaatt atatataatt tatatataat atatattata tataaattat 60

atataattta tataatatat aaattatata taatataaat tatatataat ttatataata 120

tataaattat atattatata aattaaatat aatttatatt atatataaat tatatttaat 180

ttatataata tataaattat atttaattta tatataatat aaattatatt tttatatatt 240

atgtataatt tatatattta tacatatata cattataata tattgtatag tatatataat 300

atatagtata tataaagcat a 321

<210> 197

<211> 361

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(361)

<223> MAR of chromosome 2 genomic contig; 8124469..8124829

<400> 197
tatatataat atatattata tatattatat aaattatata taatatgtaa tataaatttt 60

gtaatataaa ttatatatat aaattatata taatatatat taatatatat aatataaatt 120

aatatatata atatataatt atatataatt tatatgatat atataaatat atattatata 180

taaattatat atatcataaa ttatatatca tataaattat atataatata cattatgtac 240

ataatatatg atatataata tataatatat attatatata attatatata tataattata 300

taatatatat aaattataat atataatata tataaattat aatatataat atatataaat 360

t 361

<210> 198

<211> 418

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(418)

<223> MAR of chromosome 2 genomic contig; 11151485..11151902

<400> 198
atgtaactat atatatagta tatatagtat atatatacta tatagtgtgt atatatagta 60

SEL PCT 012.ST25

tatatatact atatagtgtg tatatatagt atatatatag tgtatatatc gtatatacac 120

tatatactat atagtgtata tatagtatat gtagtatata tagtatatat agtatagtat 180

atatagtata tatagtgtat atatactgta tatatagtgt acatagtata ctatatagta 240

tacatatagt acactgtata gtatatatag tatagtatat atagtataca tagtatacta 300

tatatagtat agtatacata gtatactata tagtatatag agtatatata cagtatacta 360

tatagtatat agagtatata tacagtatac tatatcgtgt gtatagagta tatataca 418

<210> 199

<211> 394

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(394)

<223> MAR of chromosome 2 genomic contig; 13591477..13591870

<400> 199

ttatatatat tttatatata ttatatatat tttatatata ttatatatat attatatata 60

tattatatat aattatatat aatatatatt atatatatta tatataatta tatataatat 120

atattatata tattatatat ataatatata tataatatat atattttata tatgtattat 180

atatatttta tatatattat atatattata tatatatttt atatatatta tattttatat 240

atataatata acatatataa tatataatta tatattatat atatattata ttatatataa 300

tatatattat atataatata atatataatt atatatatta tatattttat atatttatat 360

aaaaattatt ttatattatt ttatatataa atat 394

<210> 200

SEL PCT 012.ST25

<211> 1194

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1194)

<223> MAR of chromosome 2 genomic contig; 14996824..14998017

<400> 200
taatatttat atatacatat aaaatttata tataatatat aatatttata tatacatata 60

aaatttatat atatatataa tatttatata tacatataaa atttatatat aatatataat 120

atttatatat acatataaaa tttatatata atatataata tttatatata catataaaat 180

ttatatataa taaatattta tatatacata taaaatttat atataattta tatataacat 240

ataatattta tatataaaat ttatatataa catatattta tatataattt atatataaca 300

tataatattt atatataata tatatttatt tatacaattt atatataata tataatactt 360

atatatacat acataattta tatgatatat attatatata taatttatat gatatataat 420

atatctaata tatattatat atattatata tattatatat aatttatata atatatatta 480

tatatataat ttatataata tatatattat atatataatt tatataatat atatattata 540

tatataattt atataatata tattatatat ataatttata taatatatat tatatatata 600

atttatataa tatatattat atataattta tatataacat attttatata catatataat 660

ttatatataa tatatattta catatacata tataattttt atataatata aaatatttct 720

atatacatat ataatttta tataatataa aatatttcta tatacatata taatttttat 780

ataatatata tttctatata catgtctaat ttttatataa tatatatttc tatatacata 840

tataattttt atataatata taatattttt atatacataa ttttttatata atatatattt 900

SEL PCT 012.ST25

acatatacat atataatttt tatataatat atatttatat atacatatat aatttttaca 960

taatatatat tatatataca tatataattt atatacaaca tataatatat acatatataa 1020

tttatataca acatataata tttatgtata catatataat gtatacacaa tatataatat 1080

ttatatatac atatataatt tatatgtaat atatacatat ataatttata tgtaatatat 1140

atacatgtat aatttatatg tagtatatat acatgtataa tttatatgta gtat 1194

<210> 201

<211> 487

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(487)

<223> MAR of chromosome 2 genomic contig; 14998429..14998915

<400> 201

tagtatacat ttacacatac atgtataatt atatgtaata tataatattt acatatataa 60

ttatagataa tatatattta catatacata tataattata tataatatat aatgtttaca 120

tatacataca taattatata taatatatat ttaaatatac atatacaatt atatataata 180

tatatttaca tatgcatata taattataga taatatatat ttacatatac atatataatt 240

atatataata tataatgttt acatatacat atataattat atataatata tatttaaata 300

tacatataca attatatata atatatattt acatatgcat atataattat agataatata 360

tatttacata tacatatata attatatata atatataata tttacatata catatataat 420

gtatatataa tatataatat ttacatatac atatataatt tatatataat atatattata 480

tatatta 487

SEL PCT 012.ST25

<210> 202

<211> 421

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(421)

<223> MAR of chromosome 2 genomic contig; 16562490..16562910

<400> 202
tatatgaata tatatatgaa tatatacgta tatatgaata tatacatgta tgtatatatg 60

aatatatgta tatatatgaa tatatatgta tatatgaata tatgtatata tatgaatata 120

tatgtatata tgtatatata tgaatatata tgtatatatg tatatatatg aatatatatg 180

tatatatgta tatatgtata tatatgaata tatatgtata tatgaatata tatgaatata 240

tatgtatata tatgaatata tatgaatata tgtgtatata tatgaatata tatgtatata 300

tatgaatata tgtatatata tatgaatata tatgtatata tgtatatatg aatatatatg 360

tgtatatgaa tatatatatg aatatatatg tgtatatgaa tatatatgaa tatatatgtg 420

t 421

<210> 203

<211> 479

<212> DNA

<213> Homo sapiens

<220>

SEL PCT 012.ST25

<221> misc_binding

<222> (1)..(479)

<223> MAR of chromosome 2 genomic contig; 21592301..21592779

<400> 203
tatatgtata cgtatataat atattatata ttatatacgt gtacgtatat atgtaatata 60

taatgtatat gtacacgtat ataatatata atatattata tacgtatacg tatacattat 120

atattacata tatacgtata tacgtatata aaatatatgt atatattata tatacgtata 180

taatatatat tatataatat ataatatata cgtatacata taatatatta tatatacata 240

ttatatatta tatatttaaa ttatatatta tatcatatat aatatatatg atataatata 300

taatatacat atattacata atatatatta tatacatata catatataat atataatata 360

ttatatacat atacatatat aatatataat atattatata catatacata tataatatat 420

aatatattat atacatatac atatataata tataatatat tatatataca tattatata 479

<210> 204

<211> 870

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(870)

<223> MAR of chromosome 2 genomic contig; 22557584..22558453

<400> 204
tataatatat aatatacata atatgtatat tttatacaca atataaataa tatacataac 60

SEL PCT 012.ST25

atatatgtat attttatata tgtatatttt atatatattt tatatatttt atatatatgt 120

atattttata tataatatat atattgtata taataatata taatatatta tattatatat 180

aatatatata atatatatat aaatatatat tatatataat atgtataata tataatattt 240

tatatataat atgtataata tatattttat atataataat atgtacaata tatattttat 300

atataataat atgtacaata tatattttat atataataat atgtacaata tatattttat 360

gtataatatg tataatatat attttatgta taatatatat tttatgtata atatatattt 420

tacgtatatt ttatatataa tatataatat tttatatata atatataaca ttttatatat 480

aatatataat attatatata ttatatattt tatatataat atatataaat atatatattt 540

tatatataat atattttata tataatatat ataaatatat atattatata taatatattt 600

tatatataat atattttata tataatatat aatatatttt atatattata tataatatat 660

tatatattat atataatata ttatatataa tatataatat ataatatatt atatataata 720

tataatatat aatatattat atataatata taatatataa tatataatat attatatata 780

atatataata tgtaatatat aatattttat atataatata taatataata tataatattt 840

tatatataat atataatata taatatataa 870

<210> 205

<211> 1086

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1086)

<223> MAR of chromosome 2 genomic contig; 30591960..30593045

<400> 205

SEL PCT 012.ST25

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tatatattat atataaatat ataatatata tttataattt ataattataa atatatttat 120

aatatatttt tctaaatatt tatatattat atattatatc taatgatata taataaatat 180

atttctaata tattttatat ttataaaatat tttatatata ttatatattt tatatatact 240

atatattata tattatatat tttatatata ctatatatta tatagtatat attttatata 300

tactatatat tatatattat atattttata tatactatat attatatatt atatatttta 360

tatatactat atactattta ttatatattt tatatatact atatactatt tattatatat 420

tttatatata ctatatacta tttattatat attttatata tactatatat tatatattat 480

atattttata tataatatat atttattata tattttatat attatatata ttatatatta 540

tatatttata tattatataa tatatattat atatagaata tataatatat attatatata 600

atataatata atatatatta tataaaatat atataatata taaaatatat aatatatgat 660

atatataata tatattctat atttatacat atatatttaa tattatatta atatataatt 720

atatattatc atatgtaata atagatataa tatgtaatat ataaattata attatatatt 780

aatattatat attatttaat atgtatattt acacatatat taattattaa atatatatat 840

ttaatatatt aaatattatg tattaaatat atataatata tttataaata ttttatatat 900

aatatataca tatattaaca tatatgtata tatgtatata ttatatataa cattatatat 960

attatgttac atatactata ttttatatgt tacatatact atatattata tgttacatat 1020

aatatatata acatatatta taatatgtaa catattatat ataacatata atatatagta 1080

tatata 1086

<210> 206

<211> 406

<212> DNA

<213> Homo sapiens

<220>

SEL PCT 012.ST25

<221> misc_binding

<222> (1)..(406)

<223> MAR of chromosome 2 genomic contig; 36233909..36234314

<400> 206
attataaata tatattatag atattagata ttatagatat aatatatata atatatatta 60

tagatattat agatatagat ataatagata ttatagatat tatagatata atatatatta 120

tagatattat agatataata tatattatag atattataga tataatatat attatagata 180

ttatagatat aatatatatt atagatataa tatatattat agatattata gatatagata 240

ttatagatat tatatatatt atagatataa tatatattat agatattata gatatagata 300

ttatagatat aatatatatt atagatatta tagatataat atatattata gatattatag 360

atataatata tattatagat ataagatata ttatagatat tacaga 406

<210> 207

<211> 797

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(797)

<223> MAR of chromosome 2 genomic contig; 36271745..36272541

<400> 207
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tgtatatata ttatattata catatattat atatatatta tattatacat atatacatac 120

acacataaac atattacata catatacaaa ttatacacat atacatatat acatatatgt 180

atatacatac attatatata aatatatgta tataaaatgt acattatata tacatatata 240

ttatgtataa ataatatata aaataaacat aatatatatt tatagatatg atatatataa 300

tatatatgta tacatatata catatatgta tatataatgt acattataca tacataaaca 360

tcatatataa atgttatata tataatataa atatatataa tatataatat atactttata 420

tactatatat aatatatata atatgatata acatatacta tatatactat atataatata 480

tactatatat actgtatata atatataata taatatatac tatatatact aaatataata 540

tacataatat aatatatact atatataata tataatatat aatatagtat atatactata 600

tataataatt acatattata tattatacat tatatattat ataattatta tatataatta 660

tatattacat actttgtata taatgtaaat atacattaga atatataatg tatatatatg 720

tacatatata atgtatatat gtatacatta tataaactat atataaacat tatattatat 780

aaacattata tataaac 797

<210> 208

<211> 423

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(423)

<223> MAR of chromosome 2 genomic contig; 36498521..36498943

<400> 208

tattatatta tatatttaat attatatatt taatatatta tatatttaat attatatatt 60

taatatatta tatatttaat attatatatt taatatatta tatatttaat attatatata 120

SEL PCT 012.ST25

taatatatta tatatttaat attatatata taatattata tatataatat tatatattta 180

atattatata tataatatta tatatataat atattatata tttagtatta tgtatttaat 240

atattatata tttagtatta tgtatttaat atattattta tttagtatta tatatttaat 300

atattattta tttagtatta tatatttaat atattatata tttaatatat tatatattta 360

ttatatattg tatatttaat atattatata tttattatat attatatata attatatatt 420

taa 423

<210> 209

<211> 304

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(304)

<223> MAR of chromosome 2 genomic contig; 37179891..37180194

<400> 209

gtgtatatat atcatatata ttatatcata tatatgtgta tatatatcat atattatatc 60

atatatatgt gtatatatat catatatata tcatatatgt gtatatatca tatatattat 120

atatcatata tgtgtatata tatcatatat tatatatcat atatatgtgt atatatcata 180

tatattatat atatctcata tgtgtatata tatcatatat aatatatatg tgtatatatc 240

atatatcata tataacatat atatgtgtat atatcatata tataacatat atcatatatg 300

tgta 304

<210> 210

<211> 693

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(693)

<223> MAR of chromosome 2 genomic contig; 38440448..38441140

<400> 210
tatatattct tttatatatt atatataata tatattcttt tatatattat atatagtata 60

tattctttta tatattatat atagtatata ttcttttata tattatatat agtatatatt 120

cttttatata ttatatatag tatatattct tttatatatt atatatagta tatattcttt 180

tatatattat atatagtata tattctttta tatattatat atataatata tattctttta 240

tatatcatat ataatatata ttcttttata tattatatat aatatatatt cttttatata 300

ttatatatca tgtatatata atatacaaaa tatatataga ttttatatat agattattac 360

ataatagaat atattatata ttatatataa tatatacata atatataata ttatatatga 420

tataatatat atcatatata tcatataata tatattatat atcatatatt atatataata 480

atatatagat tatatataat tatatatata atatatataa ttatatatat tatctatata 540

tagataatat atataattat atataatata ttatatagat tatatataat tatattatat 600

acaaaatcta tatataatat atattatatt atatataata tacataacta tataaaaaat 660

ataatatata atatatataa tatataatat ata 693

<210> 211

<211> 471

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(471)

<223> MAR of chromosome 2 genomic contig; 38887582..38888052

<400> 211
aacatatata ctatatatat tatatactat attatatatt atatatataa acatatatac 60

tatatataat atataaacat attatattat acatgatata gataaacata tatattatat 120

ataatataga taaaatatgt tatatataat ataatgtata gacatatatt atatatacat 180

atattctaca tatattatat atatattcta cacatattat attatatata catatattct 240

acatatatta tatatacata tattctacat atattatata tacatatatt ctacatatac 300

atatatacat atattatata tacatatatt atagatatat aatatataaa catatataat 360

attattatat ataatatata taataatatt atataatata taataatatt atatcttata 420

tataaataat atatatattt tatatatata atattatata tatataatat a 471

<210> 212

<211> 1221

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1221)

<223> MAR of chromosome 2 genomic contig; 43885944..43887164

SEL PCT 012.ST25

<400> 212
catataaaca tatattatat gtaacatata aacatattat atgtaacata taatatataa 60

tatataaaca tatattttat atattatatg ttacatataa tatataatat ataaacatat 120

attatatatt atatgtaaca tataatatat aatatataaa catatatttt atatataata 180

tataaacata ttttatatat aatatataaa catattttat atataatata taaacatata 240

ttttatatat aatatataaa catattttat atataatata taaacatata ttttatataa 300

tatataaaca tataatatat ataatatata aaagtatata atataaatat atataatata 360

aacatatata atataaatat atataaaata taaacatatg taatatataa acatatatta 420

tatataatat ataaacatat attatacgta caatatataa acatatattg tacgtacaat 480

atataaacat atattatacg tacaatatat aaacatatat tatacgtaca atatataaac 540

atatattata cgtacaatat ataaacatat attatacgta caatatataa acatatatta 600

tacgtacaat atataaacat atattatacg tacaatatat aaacatatat tatacgtaca 660

atatataaac atatattata cgtacaatat ataaacatat attatacgta caataaacat 720

atattatacg tacaatatat aaacatatat tatacgtaca atatataaac atatattata 780

cgtacaatat ataaacatat attgtacgta caatatataa acatatatta tatgtataat 840

atataaacat ataatatata atatatatta tatatatgtt tattatatat gtttatatat 900

tatatataac atatattatt atattatata tgtttatata ttatatatta tataatatat 960

atgtttatat attatatatt atataatata tatgtttata tattatatat tatataatat 1020

atatgtttat atattatata ttatataata tatatgttta tatattatat attatataat 1080

atatatgttt atatattata tattatataa tatatatgtt tatatattat atattatata 1140

atatatatgt ttatatatta tatattatat aatatatatg tttatatatt atataaataa 1200

taaacttaca tattttatta a 1221

<210> 213

<211> 543

<212> DNA

SEL PCT 012.ST25

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(543)

<223> MAR of chromosome 2 genomic contig; 45818200..45818742

<400> 213
tatgtatata tacatatata tttatacatg tatatatgta tatatacata tatatttata 60

catgtatata tatacatata tatttataca tgtatatata tacatatata tttatacatg 120

tatatatata catatatatt tatacatgta tgtatatata catatatatt tatacatgta 180

tgtatatata catatatatt tatacatgta tgtatatata catatatatt tatacatgta 240

tgtatatata catatatatt tatacatgta tgtatatata catatatatt tatacatgta 300

tgtatatata catatatatt tatacatgta tgtatatata catatatatt tatacatgta 360

tgtatatata catatatatt tatacatgta tgtatatata catatatatt tatacatgta 420

tgtatatata catgtatatt tatacatgta tgtatatata catgtatatt tatacatgta 480

tgtatatata catgtatatt tatacatgta tgtatatata catgtatatt tatacatgta 540

tac 543

<210> 214

<211> 463

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

SEL PCT 012.ST25

<222> (1)..(463)

<223> MAR of chromosome 2 genomic contig; 47055478..47055940

<400> 214
atacatacat atatacatat atacacatat atacatataa tacacacata tttacatata 60

tacacacata tatacatata tacatatata cacatatata catgcataca catatataca 120

tatatacaca catatacaca catatataca tatatacaca tatatacaca tatacacata 180

tatacacaca tatacatata tacacatata tacatatata catatataca cacatataca 240

catatataca tatacacata tatacacata tacatatata cacatatata cacatatata 300

catatataca catatataca tatatacaca tatatacaca catatacaca tatatacata 360

tatacatatg tatacacata tatacatatg tatacacata tatacacata tacatatata 420

catacacata tatacgtata tatgtgtata tatacacata tac 463

<210> 215

<211> 2482

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(2482)

<223> MAR of chromosome 2 genomic contig; 47492696..47495177

<400> 215
aatatatata aaatatatta tattctatgt aatatataga atatataaaa tatattctat 60

atattatata gaatatatat tttataatat atattattta tatattttta tatatttata 120

SEL PCT 012.ST25

ttatttatat atttatatat aatttatata atttatacat ataatttata tataatttat 180

ataaattata tatataattt atatataatt tatatataat ttatataaat tatatatata 240

atttatatat aatttatatg atttttatat ataatttata tataatttat ataatttta 300

tatataattt atatataatt tatataattt ttatatataa tttatataat atatatatat 360

aatttatata taatttatat aatttatata tataatttat atataattta tataatttat 420

atatataatt tatatataat ttatataatt tatatatata atttatatat aatttatata 480

atttatatat ataatttata catatttat ataatttata tatataattt atataattta 540

tatatataat ttatatatat aatttatata atttatatat atgatttata taatttatat 600

atataattta tataatttat atatataaat tatatatata atttttatat aatttatata 660

tttataattt atatatttat ataatttata tatttataat ttatatattt atataattta 720

tatatttata atttatatat ttatataatt tatatataat tattcatata tttatataat 780

ttacatataa ttatttatat attcatatat aatttatata tttatatata atttatatat 840

aattatttac atatttatat atttatatat aatttatata tatttatata taatttataa 900

ataaaatata taatatataa tatataatat tataatagat aaaatatata ctatatatta 960

tatattttac attatattta atattatatg tataatttta tatcatatat aatatatatg 1020

atatatataa ttttatatca tatataatat atatggtata tataatttta tatcatatat 1080

aatatatatg gtatatataa ttttatatca tatataatat atgatatata attttatatc 1140

atataatata tattatatat aattttatat ctacatatta tatattatat atacaatttt 1200

atatctatct ataatatata ttatatatac aattttatat ctatataata tatattatat 1260

atacttttat attatatata aaatgtatat tatatatact tttatattat atataaaatg 1320

tatattatat ataattttat tttatatata aaatgtatat tatatataat tttattttat 1380

atataaaatg tatattatat ataattttat tttatatata aaatgtatat tatatataat 1440

tttatttttat atataaaatg tatattatat ataattttat tttatataaa aaatgtatat 1500

tatatataat tttatattat atataatatg tatattatat ataattttat attatatata 1560

atatgtatat tatatataat tttatattat atataatatg tatattatat ataattttat 1620

attatatata atatgtatat tatatataat tttgtattat atataatatg tatattatat 1680

ataattttat attatatata atatgtatat tatatataat tttatattat atataatatg 1740

tatattatat ataattttat attatatata atatgtatat tatatataat tttatattat 1800

atataatatg tatattatat ataattttat attatatata aaatgtatat tatatataat 1860

tttatattat atataatatg tatattatat ataattttat attatatata atatgtatat 1920

tatatataat tttatattat atataaaatg tatattatat ataattttat attatatata 1980

aaatgtatat tatatatatt atatataaaa tgtatattat atatattata tataaaatgt 2040

atattatata tattatatat aaaatgtata ttatatatat tatatataaa atgtatatta 2100

tgtatattat atataatgta tattatgtat attatatata atgtatatta tatataatat 2160

atattatata taatgtatat tatataatat atattatata ttataatata taatatacat 2220

tatatattac atattatata taatatatta tatattatat attacatatt atatataata 2280

tattatatat tatattaaat atatatttta tatattatat attatatatt atataaaata 2340

tatatattat atattatata aaatatatat atattatatt atatattata ttaaatatat 2400

attttatata taatatatat aatatataat atataaaata tatattatat attatatata 2460

aattatatat attatatata aa 2482

<210> 216

<211> 539

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(539)

<223> MAR of chromosome 2 genomic contig; 47561069..47561607

SEL PCT 012.ST25

<400> 216
aacagtaata tatcactaat atataataat atataacagt aatatatcat taatatataa 60

tatatcatta gtatataata ttaatatata ttaatatata atatatcata tacaatatta 120

atatatatta atatataata atatattatt aatgtataat agtaatataa tatattatca 180

atatatatta ctaatatata ataatatatc gttaatatat aatagatcat taatatataa 240

tgttaatata ttatgaatag ataatatatc agtatataat attaatatat taatatatta 300

tatattattt aataatatat aatatattaa taaataatta tatattaata tagcaatata 360

ttaatatatg actgtattat attattaata tataacaata tattatatat tatataataa 420

tttattatat aatatataat aatatattat atattatata acatattaat aatacataat 480

aacattaata atatataata atgttaatat attattatat tatatattaa tatataata 539

<210> 217

<211> 336

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(336)

<223> MAR of chromosome 2 genomic contig; 52853648..52853983

<400> 217
tatatacata aaatatatat attttatata tatacataat atatatatgt atattttatg 60

tatatatcta taatatatat aatataataa aatatacata tatattttat atatatataa 120

tatacatata aaatatacat acataaaata tacatgtata ttttatgtat atataatata 180

tatataaaat atacatgtat attttatata tataatatac atgtataatt aatatacatg 240

SEL PCT 012.ST25

tatgttatat atattacatg tatattatat ataatataca tataaatttt aaatttagtg 300

tatattacat gtatattata tataatatat gtatat 336

<210> 218

<211> 406

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(406)

<223> MAR of chromosome 2 genomic contig; 54866263..54866668

<400> 218

tacgtatata aaaatgtata tttacatata taaaataaat attttatata cgtatataaa 60

atatatattt attttatata cgtatataaa atatttattt tatatatgta tataaaatat 120

ttatttttata tacatgtata ttaaatatat atttatatat gtatataaaa atatatatta 180

tatacatgta tataaaatat atattatata tgtatataaa aatatatatg tatataaaat 240

atatatatta tatagatata taaaatatat attatataga tatataaaat atatatatta 300

tatagatata taaaatatat atattatata gatatataaa atatatatat tatatagata 360

tataaaatat atatattata tagatatata aaatatatat attata 406

<210> 219

<211> 1452

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(1452)

<223> MAR of chromosome 2 genomic contig; 55113305..55114756

<400> 219
ataatatata atatatattg tatattatat tattatatat tatatattat taaatatata 60

tattatatta tatattatat aatatatatt atatataata atatagaata tataattata 120

tattatatta tatattatat aatatatatt atatataata atatagaata tataattata 180

tattatacta tatattatat aatatatatt atatataata atatagaata tataattata 240

tattatataa tatgtgaata atgtaatata taattatatt atttacatat tatataatat 300

ataattatat tatataatat ataattatat tatttgtata ttatatataa catatacatt 360

atattatata taatataatt atatataatt aattataaat taattatata taattatata 420

atataatata taatatacat aatatataat atataataca taatatacat aatataatat 480

atattatata taatataata tatataatat aatataatat aatgtataat ataattatat 540

attatatata atatataatg ttatataatt atattatatt atataattaa ttatatgtaa 600

ttaatataat ataattatta tatataattt tttatataat ataatatata attatataat 660

ataatataat tatattatat tatataatat atatatatta tataatataa tataattata 720

ttatataatt atataatata atataattat atattatatt atataataaa tataattata 780

taatataata tgattatata atatattatg tatattatat attatatatt gtattatgta 840

tattatatat tatatattat gtatattata tattatgtat attatatatt atgtatatta 900

tatattatat attatattat gtataatata ttatgtatgt tatatataat ataaattata 960

ttatatatta tgtatattat atataaatta tattatatat tatgtatatt atatataata 1020

taaagtatat attatgtata ttatatataa tataaagtat atattatgta tattatatat 1080

aatataaagt atatattatg tatattatat ataatataaa gtatatatta tgtatattat 1140

SEL PCT 012.ST25

atataatata aagtatatat tatgtatatt atatataata taaagtatat attatgtata 1200

ttatatataa tataaagtat atattatgta tattatatat aatataaagt atatattatg 1260

tatattatat ataatataaa gtatatatta tgtatattat atataatata aagtatatat 1320

tatgtatatt atatataata taaagtatat attatgtata ttatatataa tataaagtat 1380

atattatgta tattatatat aatataaagt atatattata tgttataaat tatatattgt 1440

tatatattat at 1452

<210> 220

<211> 502

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(502)

<223> MAR of chromosome 2 genomic contig; 56350637..56351138

<400> 220

atatattata gaaatataaa tatatagata tatctatata ttatagaaat ataaatatat 60

agatatatct atatattata gaaatataaa tatatagata tatctatata ttatagaaat 120

ataaatatat agatatacct atatattata gaaatataaa tatatagata tacctatata 180

ttatagaaat ataaatatat agatatacct atatattata gaaatataaa tatatagata 240

tatctatata ttatagaaat ataaatatat agatatatct atatattata gaaatataaa 300

tatatagata tatctatata ttatagaaat ataaatatat agatatatct atatattata 360

gaaatataaa tatatagata tatctatata ttatagaaat ataaatatat agatatatac 420

aacatatatg ttacatatta tatattatat atctatatat ctatataaca ttatatatct 480

atatatctat ataacatata ta 502

<210> 221

<211> 794

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(794)

<223> MAR of chromosome 2 genomic contig; 57051633..57052426

<400> 221
aactatatat actatattat atagttatac tatatatact atattatata gttatataac 60

tattatataa ctgtattata tagttatata actattatat aactgtatta tatagttata 120

taactattat ataactgtat tatatagtta tataactata ttatataact gtgttatata 180

gttatatatt atataactat attatataac tgtattatat agttatatat tatataacta 240

tattatataa ctgtattata tagttatata ttatataact atattatata actgtattat 300

atagttatat attatataac tgtattatat agttataaaa ctatattata taactgtatt 360

atatagttat aaaactacta tataactgta ttatataatt ataaaattat actatataac 420

tgtattatat agttataaaa ctatactata taactgtatt atatagttat aaaactatac 480

tatataactg tattatatag ttataaagct atactatata actgtattat atagttatat 540

aactatacta tataactgta ttatatagtt ataaaactat actatataac tgtattatat 600

agttataaaa ttatattata taactgtatt atatagttat ataactatat tatataactg 660

tattatatag ttatataact atattatata agtgtattat atagttatat aactatatta 720

tataactgta ttatacagtt atataactat attatataac tgtattatat acttatataa 780

ctatattata taac

<210> 222

<211> 300

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(300)

<223> MAR of chromosome 2 genomic contig; 57069272..57069571

<400> 222
acacatacat atatgtatat atgcacacac atatatatgt atatatacac atacatatat 60

gtatatatac atatatgtat atacgcacat acatatatgt atatatacac gtacatatat 120

gtctctatat atacacatac acatatgtat atacatatat gtgtatatat acacaatcat 180

atatgtatat acatatatac acatatacac aaacatatat gtatatacat atatgtatat 240

acatatatac acatatacac aaacatatat gtatatacat atatgtatat acatacacaa 300

<210> 223

<211> 370

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(370)

SEL PCT 012.ST25

<223> MAR of chromosome 2 genomic contig; 57235143..57235512

<400> 223
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atcatatata taatcatata tgattatata tgatcatata tatatttata tatataatta 120

tatatactta tatataatta tatatatatt tatatatata attatgtata cttatatata 180

tttatatata taattatata tacaatttat atatataatt atatataatt tatatataat 240

tatatatata aattatatat aagtatatat aattatatat atgtttatat ataattatat 300

atataaatga tatgtataat atataactat atataattat atataaatat atatatagat 360

tttatatata 370

<210> 224

<211> 306

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(306)

<223> MAR of chromosome 2 genomic contig; 57693125..57693430

<400> 224
tacgtatata cacgtataaa tataaatata tacatgtata tacgtatata catgtataaa 60

tataaatata tatatgtata tacgtatata catgtataaa tatatatatg tatatacgta 120

tatacatgta taaatatata tatatgtata tacgtatata catgtataaa tatatataca 180

tgtatatacg tatgttgtgt atacatacaa atctgtacat atatacatat atgttgtgtg 240

SEL PCT 012.ST25

tatatataca tctatacatg tgtatgcgta tatatgtata tgtatatata gtatatataa 300

tacatg 306

<210> 225

<211> 500

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(500)

<223> MAR of chromosome 2 genomic contig; 59810331..59810830

<400> 225

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attatatata ttatatataa tatatattgt attattatat atattatata taatatatat 120

tgtattatta tatatattat atataatata tattgtatat tatatatatt atatattata 180

ttattatata ttatatatat tatattatta tatattatat attatatata ttatattata 240

tattatatat tatattatat atattatatt atatattata tattatatta tatatattat 300

attatatatt atatattata ttatatatat tatattatat atattatata ttatatatta 360

tatatattat atattatata ttatatatat tatatattat atataatata tattatatta 420

ttatataata ttatatatta tatatattat atattatata taatatatat tatattatta 480

tataatatta tatattatat 500

<210> 226

<211> 565

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(565)

<223> MAR of chromosome 2 genomic contig; 59974589..59975153

<400> 226
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atgtatatat tatatatcat atataatata taatgtgtat atatgtatat atgtatgtat 120

acatgtatat actatgtata tattgtatat attatatatg tatatataca tatacatata 180

taatatatac atatattata tacaatatat acatgtatat tatatacgat atatacatat 240

atattatata caatatatac atagtatata aatgtataca tacatacata tatacatatt 300

atatatgtat atatgtatac ataaatgtat atataatata tatacatata taaatgtata 360

catacgtaca tatacgtata tgtatatgca tatatgtata tatgtgcata catatatatg 420

tatatacata tatgtacata tgtacatata cgtatatatg tacatatgta catatacgta 480

tatatgtaca tatgtacata tacgtatata tgtacatatg tacatatacg tatatatgta 540

catatgtaca tatatacata tatat 565

<210> 227

<211> 427

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

SEL PCT 012.ST25

<222> (1)..(427)

<223> MAR of chromosome 2 genomic contig; 60605573..60605999

<400> 227
tatataatgt atataatgga tatagatata gatatagata tatattttat ataatatata 60

ttatatatta tatataatat atgttatata tattatatat tttataaat atatatatta 120

tataaattat atatatataa tatataatat atatattata tatattttat ataatatata 180

tttaatatta tctattatat attttatata atatatattt tatataatat ataatatata 240

atatatattt tacataatat ataatatata atacgtatta tatataatat ataatacgta 300

ttttatataa tatataatac gtattatata taatacgtat tatatattat ataatatata 360

atacgtatta tataatatac gtaattatat tttattataa tacgtattat atattatata 420

atatata 427

<210> 228

<211> 1199

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1199)

<223> MAR of chromosome 2 genomic contig; 61229949..61231147

<400> 228
gtatacatat ataaagtgta tatataatgt atatacatat atacatatat aaagtatata 60

tataatatat acatatataa agtatatata taatatatac atatataaag tatatataat 120

SEL PCT 012.ST25

atatacatat ataaagtata tataatatat acatatataa agtatatata tcatatatac 180

atatataaag tatatatata atatatacat atatacatat ataaagtata tataacatat 240

atacatatat aaagtatata taacatatat acatatataa agtatatata taatatatac 300

atatatacat atataaagta tatataacat atatacatat atacagtata tataacatat 360

atacatatat acagtatata taacatatat acatatatac agtatatata acatatatac 420

atatatacag tatatataac atatatacat atatacatga agtatatata acatatatac 480

atatatacat gaagtatata taacatatat acatatatac atgaagtata tataacatat 540

atacatatat acatgaagta tatataacat atatacatat atacatatat aaagtatata 600

taacatatac atatatacat atataaagta taacatatac atatatacat atataaagta 660

tatataatat ataacatata catatataaa gtatatataa tatataacat atacatatat 720

aaagtatata taatatataa catatacata tataaagtat atataatata tacatatata 780

catatataaa gtatatataa tatatatata catatataaa gtatatataa tatatataca 840

tatatacata tataaagtat atataatata tatacatata taaagtatat ataatatata 900

tacatatata catatataaa gtatatataa tatatataca tatatacata tataaagtat 960

atataatata tatacatata tacatatata aagtatatat aatatatata catatataca 1020

tatataaagt atatataata tatatacata tatacatata taaagtatat ataatatata 1080

tacatatata catatataaa gtatatataa tatgtataca tatatacata tataaagtat 1140

atataatatg tatacatata tacatatata aagtatatat ataatatgta tacatatat 1199

<210> 229

<211> 454

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(454)

<223> MAR of chromosome 2 genomic contig; 62181058..62181511

<400> 229
tatatatcat atattatata tgatatatat tatgtatata atacatatta tatataataa 60

atatttatta tatatgatat atattatgta tataatacat attatatata ataaatatat 120

attatattat atataataaa tatatattat attatatata atatatattt atatataaat 180

atattatata taaatatata ttatatataa aatatttata tattatatat aaatatatat 240

tatatataaa tatttatata ttatatataa atatttatat attatatata aatatttata 300

tattatatat aaaatatatt atatatatta tatatattat atattatata taatatattt 360

aatatataat atataaacat atattatata taatatataa acatatataa atatatttat 420

atataatага taaaaatata tataatatat ataa 454

<210> 230

<211> 658

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(658)

<223> MAR of chromosome 2 genomic contig; 62190919..62191576

<400> 230
tatatacaca actatatata taactatata tatacaacta tatatacaac tatatatata 60

actatatata taactatata taactatata tataactata tatataacta 120

SEL PCT 012.ST25

tatatataac tatatataac tatatatata actatatata actatatata 180

taactatata tataactata tatataacta tatatataac tatatatact atatatataa 240

ctatatatat ataactatat atataactat atatatataa ctatatataa ctatatatat 300

ataactatat atataactat atatatataa ctatatatat aactatatat atataactat 360

atatataact atatatatat aactatatat aactatatat atataactat atatataact 420

atatatatat aactatatat ataactatat atatataact atatatataa ctatatatat 480

ataactatat atataactat atatataact atatatataa ctatatatat ataactatat 540

atataactat atatatataa ctatatatat aactatatat ataactatat atataactat 600

atatatataa ctatatatat aactatatat atataactat atatataact atatatat 658

<210> 231

<211> 1486

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1486)

<223> MAR of chromosome 2 genomic contig; 62384127..62385612

<400> 231

attatatcta atctattata tattatatct aatacatatt atatctaatc tattgtatat 60

tatatctaat atataatata ttatatataa tatattatat attatatatt atatacaata 120

tattatatat tatataatat ataatatatt atatataata tattatatct aatatattac 180

atattatatc taatctatta tagatataat atgtaatata ttatatatta tatctaatag 240

atattagata taatatataa tatattatta atataatata ttagatataa tatataatat 300

SEL PCT 012.ST25

aataatatat aatatatatt attggtaata tataatatat aattaataat atatattata 360

tataattatt atgaataata tatcatatat aatatctagt atattatata ttaataacat 420

ataaatatta tattaataat aaataacata ttaatattat attaataata tataatatac 480

taatattata ttaataatat ataatatact aatattatat taataatata taatatacta 540

atattatatt aataatatat aatatactaa tattatatta ataatatata atatactaat 600

attatattaa taatatataa tatactaata tattaagaat atataatata ctaatatatt 660

aagaatatat aatatactaa tattatatta ataatatata tttatattaa taatatatta 720

attattatta attaattatt aataattata taatattgat tatattaata ttatcaattt 780

aataatattg attatatatt atatattata tattatatat tatatattat atattatata 840

ttatatatta ataatatata ttagatataa tataatatat taataatata taagatataa 900

tataatatat taataatata tattagatat aatataatat attaataata tatattagat 960

ataatataat atattaataa tatatattag atataatata atatattaat aatatatatt 1020

agatgtaata taatatatta ataatatata ttagatgtaa tataatatat taataatata 1080

tattagatgt aatataatat attaataata tatattagat gtaatataat atattaataa 1140

tatatattag atgtaatata atatattaat aatatatatt agatgtaata taatatatta 1200

ataatatata ttagatgtaa tataatatat taatatatat tagatgtaat ataatatatt 1260

aataatatat attagatata atataatata ttaataatat attagatata atataatata 1320

ttaataatat ataagatata atataatata ttaataatat ataagatata atataatata 1380

ttaataatat ataagatata atataatata ttaataatat atattagata tataatatat 1440

taataatata tattagatat ctaatatcta ttagatatct aataga 1486

<210> 232

<211> 333

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(333)

<223> MAR of chromosome 2 genomic contig; 62538649..62538981

<400> 232
ttatatatat tatatatata tattttatat atatattata tatatatttt atatatatat 60

tatatatata ttttatatat atattatata tatattttat atatatatta tatatatatt 120

ttatatatat tatatatata ttttatatat attatatata tattttatat atatattata 180

tatatatttt atatatatat tatatatata ttttatatat atattatata tatattttat 240

atatatatta tatatatatt ttatatatat attatatata tattttatat atatattata 300

tatatatttt atatatatat tatatatata ttt 333

<210> 233

<211> 480

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(480)

<223> MAR of chromosome 2 genomic contig; 63240325..63240804

<400> 233
tatatataaa atatatattt tttaaatata aaatatatat atattttaat attaatatat 60

atatatttta atatataata tatatattat atattttata tataaaatat atatattata 120

SEL PCT 012.ST25

tattttatat ataaaatata tatattatat attttatata ttaaaatata tattttatat 180

attttaatta ttaaaatata tatattatat attttaaata taaaatatat atattatata 240

ttttaatata taaaatatat atattatata ttttaatata taaaatatat atattttata 300

tttatatata taaatatata tattatatat tttaatatat aaaatatata tattatatat 360

tttaatatat aaaatatata tattatatat tttaatatat aaaatatata tattatatat 420

tttaatatat ataaaatata tatattatat attttatata tattaaatat atattttata 480

<210> 234

<211> 302

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(302)

<223> MAR of chromosome 2 genomic contig; 63935480..63935781

<400> 234

atatatataa atatatatat aattatatat agatatatat aattatatat agatatatat 60

attctatatt ctatatatat ataatatata atatataaat tatatataga atatatatta 120

tatataatat attatatata ttatatataa tatatatatt atatatatta tatataatat 180

atatattata tatattatat ataatttata tatattatat atagaatata tattatatat 240

agaatataga atatatataa tatatataga atacagaata tatatagaat atagaatata 300

ta 302

<210> 235

<211> 407

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(407)

<223> MAR of chromosome 2 genomic contig; 63935888..63936294

<400> 235
tataatatat taatataata tatagacagt atataatata atatacagac agtatataat 60

atacagacag tatataatat ataatattat atataatatt atatataata ttatataata 120

tattatatta tatatattat ataatatatt atattatata taatatatgt aatattatat 180

attatattat acataatata ttatatataa tatattatat ataatattat atatattata 240

tataatatat ataataataa tattataata tataatatat aatagtacag tatatattat 300

atatataatt ctatatataa tatatagaat tctatctatt tataatatat atagaattct 360

atatataata tataatatac agaattctat atatattata tatagaa 407

<210> 236

<211> 302

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(302)

<223> MAR of chromosome 2 genomic contig; 66958350..66958651

<400> 236
tattatatat attgtatata tatgtatatt atatatattg tatataaat gtatattata 60

tatattatat atatatgtat attatatata ttgtatatat atgtatatta tatatattgt 120

atatatgtat atgtatatat gtatgtgtat atatatacac atatacacat atatgtgtat 180

gtatatatat gtgtgtatat acgtatatat acatatatac aatttttgta tatatacata 240

tatacacata tatatgtgta tgtgtatata tatacacata tatgtgtgtg tatatacaca 300

ta 302

<210> 237

<211> 651

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(651)

<223> MAR of chromosome 2 genomic contig; 68307125..68307775

<400> 237
gatattatat attgtatata ttatatatgt atataatata ctattatata ttatatatgt 60

atataatttt attaatatat atattatatt atattatata ttatattata ttatattata 120

tatataatat taatattata tattattata tattatatta tattaatatt atatatatat 180

aatatatata atatatataa tagtattata tataatatat ataatagtat tatatattat 240

atatatataa tactattata tatattatat ataatagtat tatatatatt atatatataa 300

tactattata tataatatat actattatat aatatatata atactattat atatattata 360

SEL PCT 012.ST25

tataatacta ttatatataa tatatataat actattatat ataatatata taatactatt 420

atatataata tatataatac tattatatat aatatatata atactattat atataatata 480

tataatacta ttatatataa tatatatatt atatataatt atattaatat ataatagtat 540

catatataat aatagtatat ataatatata atatatatat tatatatatt ataatagtat 600

atataacata taatatagta tatatattat atattatata taaaatattt a 651

<210> 238

<211> 367

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(367)

<223> MAR of chromosome 2 genomic contig; 68308243..68308609

<400> 238

atatatatat atgagtcaac catacacata tatatatata atgtttatat atataatgta 60

tatatataat gtttatatat aatgtatata tataatgttt atatatataa tgtatatata 120

taatgtttat atatataatg tatatatata atgtttatat atataatgtg tatatataat 180

gtttatatat ataatgtgta tatataatgt ttatatataa tgtgtatata taatgtttat 240

atatataatg tgtatatata atgtttatat atataatgtg tatatataat gtttatatat 300

ataatgtgta tatatataat gtttatatat ataatgtgta tatatataat gtttatatat 360

ataatgt 367

<210> 239

<211> 499

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(499)

<223> MAR of chromosome 2 genomic contig; 410241..410739

<400> 239
ataatatgta tatatattat attatatatt atattacata ttatatatta tattacatat 60

tatatattta tatattacat attatatatt atattttata ttatatatta tatcatatat 120

atgttatgca ttatataata cataatatat tatatatgat ataatatata ttatatatta 180

ttatatataa tataattaat atattatgta ttatataata tatattatgt tataatatat 240

aatatatatt atataattat ataatatatt atgtattata taatatatat tatgttataa 300

tatattatat tatatatatt atatatatat tatatatata atgtatatta tatataatac 360

ataatatatt atatattata tattatttta tataatatat tatataatgt gatatattat 420

ataatatatt atataacata gtatattata taatatatta tataatgtaa tatattatat 480

attatataat atattgtat 499

<210> 240

<211> 402

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

SEL PCT 012.ST25

<222> (1)..(402)

<223> MAR of chromosome 2 genomic contig; 31531..31932

<400> 240
cacattatat atataaacat tatatatata cacattatat atataaacat tatatatata 60

cacattatat atataaacat tatatataca cattatatat ataaacatta tatatacaca 120

ttatatatat aaacattata tatacaaatt atatatataa acattatata tacaaattat 180

atatataaac attatatata tacattatat atataaacat tatatatata cattatatat 240

ataaacatta tatatataca ttatatatat aaacattata tatatacatt atatatataa 300

acattatata tatacattat atatataaac gttatatata tacattatat atataaacat 360

tatatgtata cattatatat ataaacatta tatatatatg tg 402

<210> 241

<211> 421

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(421)

<223> MAR of chromosome 2 genomic contig; 32415..32835

<400> 241
ataaatattt tatatataat atataatata tatactatat tatatgttat atatactatt 60

ataatatata taatatatat attatatatt atatatacta ttattatata tgatactatt 120

atatattaat ataattatat ataatatata tattatataa tatactatta tatattatat 180

SEL PCT 012.ST25

ataatagtat attatataat atatatatta tatataatag tattatatat actattatat 240

attatatata ttatatatat ataaaatata atataatata tataatatat aatattaata 300

ttatatatat aatataatat aatatatataat ataatataat atatatatta ataaaattat 360

attaatatat aatatataat agtatattat atacatatat aatatataca atatataata 420

t 421